

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 13, 2003, 04:37:24 ; Search time 1703.81 Seconds
(without alignments)
7460.491 Million cell updates/sec

Title: US-09-852-261-5
Perfect score: 523
Sequence: 1 ggaccggagacgctctgcgg.....aaatacacaagtaaaccattc 523

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*

28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
c	1	364.8	69.8	558	9	AI503976	AI503976 vm43d08.x
c	2	363	69.4	623	9	AW146128	AW146128 um37e10.x
c	3	348.2	66.6	549	9	AI169253	AI169253 EST215088
c	4	347	66.3	558	9	AI265629	AI265629 uj04b07.x
	5	339.6	64.9	614	14	CD373004	CD373004 UI-R-GR0-
	6	339.2	64.9	816	9	AI119218	AI119218 ue94h02.y
	7	334.8	64.0	594	10	BF383724	BF383724 602044632
	8	334.4	63.9	796	14	CB959991	CB959991 AGENCOURT
c	9	322.2	61.6	499	9	AW495481	AW495481 UI-M-BH3-
c	10	320.8	61.3	642	9	AI876493	AI876493 uj59b10.x
c	11	320.8	61.3	673	12	BM984670	BM984670 UI-CF-EC1
c	12	316.8	60.6	575	9	AI248089	AI248089 qh69f05.x
c	13	309.2	59.1	468	9	AI169770	AI169770 EST215669
c	14	305	58.3	498	9	AA542914	AA542914 ni98c10.s
	15	299	57.2	882	9	AI604642	AI604642 vm43d08.y
c	16	296.4	56.7	653	13	BQ200567	BQ200567 UI-R-DZ1-
c	17	291.6	55.8	527	9	AA913900	AA913900 ol35g05.s
c	18	271.6	51.9	521	9	AW493459	AW493459 UI-M-BH3-
	19	271.6	51.9	559	12	BI715603	BI715603 ic34h10.y
	20	271.6	51.9	602	13	BU590710	BU590710 AGENCOURT
	21	271.6	51.9	621	12	BI221656	BI221656 602936980
	22	271.6	51.9	1658	11	AK081019	AK081019 Mus muscu
c	23	270.6	51.7	595	9	AI573421	AI573421 mo04b11.x
c	24	270	51.6	499	12	BI676839	BI676839 ic56a08.x
c	25	266.8	51.0	500	9	AA945553	AA945553 EST201052
c	26	266.8	51.0	525	9	AA963258	AA963258 UI-R-E1-g
	27	266	50.9	665	9	AA690767	AA690767 vu57d12.r
	28	265.2	50.7	559	12	BI715465	BI715465 ic33b09.y
	29	263.8	50.4	799	9	AI314558	AI314558 uj48d07.y
c	30	263.6	50.4	525	9	AI599751	AI599751 EST251454
c	31	261.4	50.0	499	12	BI294072	BI294072 UI-R-DK0-
c	32	260.4	49.8	561	12	BI714874	BI714874 ic33b09.x
c	33	258.4	49.4	502	9	AI104669	AI104669 EST213958
c	34	258	49.3	564	12	BI714981	BI714981 ic34h10.x
	35	256	48.9	2170	11	AK038119	AK038119 Mus muscu
c	36	254.8	48.7	430	9	AI478804	AI478804 tm52e04.x
	37	254.8	48.7	558	12	BI715475	BI715475 ic33c08.y
	38	250.8	48.0	512	9	AI876203	AI876203 uj59b10.y
	39	249.6	47.7	949	14	CB589117	CB589117 AGENCOURT
c	40	248.2	47.5	637	9	AW413016	AW413016 uq49h08.x
	41	246.4	47.1	473	9	AA451360	AA451360 vf84g03.r
c	42	246.4	47.1	486	9	AA993659	AA993659 ot85g11.s
	43	246.2	47.1	773	12	BI144500	BI144500 602908689
	44	243.2	46.5	482	9	AA456717	AA456717 aa13h06.r
c	45	243	46.5	474	9	AI526955	AI526955 uj48d07.x

ALIGNMENTS

RESULT 1

AI503976/c

LOCUS AI503976 558 bp mRNA linear EST 11-MAR-1999

DEFINITION vm43d08.x1 Stratagene mouse diaphragm (#937303) Mus musculus cDNA clone IMAGE:1001007 3' similar to gb:X04482 Mouse mRNA for preproinsulin-like growth factor IB (MOUSE);, mRNA sequence.

ACCESSION AI503976

VERSION AI503976.1 GI:4401827

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 558)

AUTHORS Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.

TITLE The WashU-NCI Mouse EST Project 1999

JOURNAL Unpublished

COMMENT Contact: Marra M/WashU-NCI Mouse EST Project 1999

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:565223

This clone was previously sequenced on the 5' end only, this new data is from the 3' end

High quality sequence stop: 440.

FEATURES

source

Location/Qualifiers

1. .558

/organism="Mus musculus"

/mol_type="mRNA"

/db_xref="taxon:10090"

/clone="IMAGE:1001007"

/tissue_type="diaphragm"

/dev_stage="adult"

/lab_host="SOLR (kanamycin resistant)"

/clone_lib="Stratagene mouse diaphragm (#937303)"

/note="Organ: diaphragm; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally from mRNA prepared from diaphragm muscle. Primer: Oligo dT. Average insert size: 1.5 kb. Uni-ZAP XR Vector; ~5' adaptor

sequence: 5' GAATTCGGCAG 3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"

BASE COUNT

103 a 133 c 149 g 173 t

ORIGIN

Query Match 69.8%; Score 364.8; DB 9; Length 558;
 Best Local Similarity 83.2%; Pred. No. 8.8e-81;
 Matches 441; Conservative 0; Mismatches 82; Indels 7; Gaps 2;

```

Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
      ||||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      530 GGACCGAGAGACCCTTTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGACCG 471

Qy      61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      470 AGGGGCTTTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTTCGGAGGGCACCTCAG 411

Qy     121 ACAGGCATCGTGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     410 ACAGGCATGTGTGATGAGTGTGCTTCCGGAGCTGTGATCTGAGGAGACTGGAGATGTAC 351

Qy     181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240
      ||||| || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     350 TGTGCCCCACTGAAGCCTACAAAAGCAGCCCGCTCTATCCGTGCCAGCGCCACACTGAC 291

Qy     241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
      ||||| ||||| ||||| || || || || || || || || || || || || || || || ||
Db     290 ATGCCCAAGACTCAGAAGTCCCCGTCCCTATCGACAAACAAGAAAACGAAGCTGCAAAGG 231

Qy     301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     230 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 171

Qy     361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
      ||| ||||| || || || || || || || || || || || || || || || ||
Db     170 CAGAATGTAGGAGGAGCCTCCACGGAGCAGAAAATGCCACATCACCGCAGGATCCTTTG 111

Qy     421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA-----AAAAATAAGTTTGATC 474
      ||  ||  || ||||| || || || || || || || || || || || || || || ||
Db     110 CTGCTTGAGCAACCTGCAAAACATCGAAACACCTACCAAATAACAATAAAGTCCAATA 51

Qy     475 ACATTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTTC 523
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      50 ACATTACAAAGATGGGCATTTCCCCCAATGAAATATACAAGTAAACATTTC 1
  
```

RESULT 2

AW146128/c

LOCUS AW146128 623 bp mRNA linear EST 10-OCT-2000

DEFINITION um37e10.x1 Sugano mouse embryo mewa Mus musculus cDNA clone
 IMAGE:2247498 3' similar to gb:X04482 Mouse mRNA for
 preproinsulin-like growth factor IB (MOUSE);, mRNA sequence.

ACCESSION AW146128

VERSION AW146128.1 GI:6167864

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 623)

AUTHORS Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
 Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person


```

TITLE      The WashU-NCI Mouse EST Project 1999
JOURNAL    Unpublished
COMMENT    Contact: Marra M/WashU-NCI Mouse EST Project 1999
           Washington University School of Medicine
           4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
           Tel: 314 286 1800
           Fax: 314 286 1810
           Email: mouseest@watson.wustl.edu
           This clone is available royalty-free through LLNL ; contact the
           IMAGE Consortium (info@image.llnl.gov) for further information.
           MGI:1006958
           Seq primer: custom primer used
           High quality sequence stop: 499.

FEATURES   Location/Qualifiers
source     1. .623
           /organism="Mus musculus"
           /mol_type="mRNA"
           /strain="C57BL"
           /db_xref="taxon:10090"
           /clone="IMAGE:2247498"
           /dev_stage="embryo, 14 dpc"
           /lab_host="DH10B"
           /clone_lib="Sugano mouse embryo mewa"
           /note="Vector: pME18S-FL3; Site_1: DraIII (CACTGTGTG);
           Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed
           with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTTTTTTTT];
           double-stranded cDNA was ligated to a DraIII adaptor
           [TGTTGGCCTACTGG], digested and cloned into distinct DraIII
           sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site
           CACCATGTG). XhoI should be used to isolate the cDNA
           insert. Size selection was performed to exclude fragments
           <1.5kb. Library constructed by Dr. Sumio Sugano
           (University of Tokyo Institute of Medical Science).
           Custom primers for sequencing: 5' end primer
           CTTCTGCTCTAAAAGCTGCG and 3' end primer
           CGACCTGCAGCTCGAGCACA."

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Query Match 69.4%; Score 363; DB 9; Length 623;
Best Local Similarity 81.9%; Pred. No. 2.5e-80;
Matches 433; Conservative 0; Mismatches 90; Indels 6; Gaps 1;

[illegible]

/mol_type="mRNA"
/db_xref="taxon:10118"
/clone="RKIBP33"
/clone_lib="Normalized rat kidney, Bento Soares"
/note="Organ: kidney; Vector: pT7T3Pac; Site_1: EcoRI;
Site_2: NotI"

BASE COUNT 112 a 140 c 133 g 164 t
ORIGIN

Query Match 66.6%; Score 348.2; DB 9; Length 549;
Best Local Similarity 81.8%; Pred. No. 1.3e-76;
Matches 428; Conservative 0; Mismatches 88; Indels 7; Gaps 2;

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Qy      8 AGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGACAGGGGCT 67
      ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    549 AGACCCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAATTCTGTGTGGACCAAGGGGCT 490

Qy     68 TTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAGACAGGCA 127
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    489 TTTACTTCAACAAGCCACAGGCTATGGCTCCAGCATTCTGAAGGGCACCACAGACGGGCA 430

Qy    128 TCGTGGATGAGTGTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTACTGTGCAC 187
      | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    429 TTGTGGATGAGTGTAGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTACTGTGCTC 370

Qy    188 CCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGACATGCCCA 247
      | || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    369 CGCTGAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACATTGACATGCCCA 310

Qy    248 AGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGGAGAAGGA 307
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    309 AGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGGAGAAGGA 250

Qy    308 AAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAGGATG 367
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    249 AAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACTTACAGAATG 190

Qy    368 TAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTGCTCTGCA 427
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Db    189 TAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTGCTGCTTG 130

Qy    428 CAGTTACCTGTAAACATTGGAATACCGGCCA-----AAAAATAAGTTTGATCACATTTTC 481
      | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    129 AGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATACCATTTTC 70

Qy    482 AAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTTC 523
      | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     69 AGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTTC 27
```

RESULT 4

AI265629/c

LOCUS AI265629 558 bp mRNA linear EST 18-NOV-1998

DEFINITION uj04b07.x1 Sugano mouse liver mlia Mus musculus cDNA clone
IMAGE:1890901 3' similar to gb:X04482 Mouse mRNA for
preproinsulin-like growth factor IB (MOUSE);, mRNA sequence.

ACCESSION AI265629

VERSION AI265629.1 GI:3883787
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 558)
 AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
 Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
 Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
 Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
 Waterston,R.
 TITLE The WashU-HHMI Mouse EST Project
 JOURNAL Unpublished
 COMMENT Contact: Marra M/Mouse EST Project
 WashU-HHMI Mouse EST Project
 Washington University School of MedicineP
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:975225
 Seq primer: custom primer used
 High quality sequence stop: 495.
 FEATURES Location/Qualifiers
 source 1. 558
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL"
 /db_xref="taxon:10090"
 /clone="IMAGE:1890901"
 /sex="female"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="Sugano mouse liver mlia"
 /note="Organ: liver; Vector: pME18S-FL3; Site_1: DraIII
 (CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA
 was primed with an oligo(dT) primer
 [ATGTGGCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was
 ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
 and cloned into distinct DraIII sites of the pME18S-FL3
 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
 be used to isolate the cDNA insert. Size selection was
 performed to exclude fragments <1.5kb. Library
 constructed by Dr. Sumio Sugano (University of Tokyo
 Institute of Medical Science). Custom primers for
 sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
 primer CGACCTGCAGCTCGAGCACA."
 BASE COUNT 106 a 135 c 156 g 161 t
 ORIGIN

Query Match 66.3%; Score 347; DB 9; Length 558;
 Best Local Similarity 82.0%; Pred. No. 2.5e-76;
 Matches 414; Conservative 0; Mismatches 85; Indels 6; Gaps 1;

Qy 1 GGACCGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
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 Db 506 GGACCAGAGACCCCTTTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGACCG 447
 Qy 61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
 |||||
 Db 446 AGGGGCTTTTACTTCAACAAGCCACAGGCTATGGCTCCAGCATTTCGGAGGGCACCTCAG 387
 Qy 121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
 |||||
 Db 386 ACAGGCATTGTGGATGAGTGTGCTTCCGGAGCTGTGATCTGAGGAGACTGGAGATGTAC 327
 Qy 181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
 |||||
 Db 326 TGTGCCCCACTGAAGCCTACAAAGCAGCCCGCTCTATCCGTGCCCAGCGCCACACTGAC 267
 Qy 241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
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 Db 266 ATGCCCAAGACTCAGAAGTCCCCGTCCCTATCGACAAACAAGAAAACGAAGCTGCAAAGG 207
 Qy 301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
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 Db 206 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 147
 Qy 361 CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTTG 420
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 Db 146 CAGAATGTAGGAGGAGCCTCCACGGAGCAGAAAATGCCACATCACCAGGATCCTTTG 87
 Qy 421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA-----AAAAATAAGTTTGATC 474
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 Db 86 CTGCTTGAGCAACCTGCAAAACATCGAAACACCTACCAAATAACAATAAAGTCCAATA 27
 Qy 475 ACATTTCAAAGATGGCATTTCCTCC 499
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 Db 26 ACATTACAAAGATGGGCATTTCCTCC 2

RESULT 5
 CD373004

LOCUS CD373004 614 bp mRNA linear EST 29-MAY-2003
 DEFINITION UI-R-GR0-csv-j-17-0-UI.r1 UI-R-GR0 Rattus norvegicus cDNA clone
 UI-R-GR0-csv-j-17-0-UI 5', mRNA sequence.
 ACCESSION CD373004
 VERSION CD373004.1 GI:31157094
 KEYWORDS EST.
 SOURCE Rattus norvegicus (Norway rat)
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 REFERENCE 1 (bases 1 to 614)
 AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene
 discovery
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 97044477
 PUBMED 8889548

COMMENT Contact: Soares, MB
 Coordinated Laboratory for Computational Genomics
 University of Iowa
 375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA
 Tel: 319 335 8250
 Fax: 319 335 9565
 Email: bento-soares@uiowa.edu
 Tissue Procurement: James Lin, University of Iowa
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/rat.html>
 Seq primer: M13 REVERSE.

FEATURES Location/Qualifiers
 source 1. .614
 /organism="Rattus norvegicus"
 /mol_type="mRNA"
 /strain="Sprague-Dawley"
 /db_xref="taxon:10116"
 /clone="UI-R-GR0-csv-j-17-0-UI"
 /tissue_type="Whole embryo"
 /dev_stage="embryo 13dpc"
 /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
 /clone_lib="UI-R-GR0"
 /note="Vector: pYX-Asc; Site_1: EcoR I; Site_2: Not I;
 UI-R-GR0 is a cDNA library containing the following
 tissue(s): rat whole embryo 13dpc. The library was
 constructed according to Bonaldo, Lennon and Soares,
 Genome Research, 6:791-806, 1996. Denatured RNA was size
 fractionated on a 1% agarose gel. First strand cDNA
 synthesis was primed with oligo-dT primer containing a Not
 I site. Double strand cDNA was size selected according to
 mRNA size fraction, ligated with EcoR I adaptor, digested
 with NotI and then cloned directionally into pYX-Asc
 vector. The library tag sequence located between the Not I
 site and the polyA tail is CATCTCTACT. This library was
 created for the University of Iowa Program for Rat Gene
 Discovery and Mapping (Val Sheffield, Bento Soares and Tom
 Casavant)."

BASE COUNT 171 a 168 c 154 g 119 t 2 others
 ORIGIN

Query Match 64.9%; Score 339.6; DB 14; Length 614;
 Best Local Similarity 81.4%; Pred. No. 1.9e-74;
 Matches 393; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

```

Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
          ||||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      116 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 175

Qy      61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      176 AGGGGCTTTTACTTCAACAAGCCACAGGCTATGGCTCCAGCATTTCGGAGGGCACACAG 235

Qy      121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
          || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```


Seq primer: custom primer used
High quality sequence stop: 473.

BASE COUNT	230 a	219 c	172 g	187 t	8 others
ORIGIN					

Query Match 64.9%; Score 339.2; DB 9; Length 816;
Best Local Similarity 81.2%; Pred. No. 2.5e-74;
Matches 389; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

Qy	1	GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTTCGTGTGTGGAGAC	60
Db	323	GGACCAGAGACCCCTTTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTTCGTGTGTGGACCG	382
Qy	61	AGGGGCTTTTTATTTCAAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGGCACCTCAG	120
Db	383	AGGGGCTTTTTACTTCAACAAGCCCACAGGCTATGGCTCCAGCATTCGGAGGGGCACCTCAG	442
Qy	121	ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC	180
Db	443	ACAGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGACTGGAGATGTAC	502
Qy	181	TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC	240
Db	503	TGTGCCCCACTGAAGCCTACAAAAGCAGCCCGCTCTATCCGTGCCCAGCGCCCACTGAC	562
Qy	241	ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAAATGAAGTCTCAGAGG	300
Db	563	ATGCCCAAGACTCAGAAGTCCCCGTCCCTATCGACAAACAAGAAAAACGAAGCTGCAAAGG	622
Qy	301	AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA	360
Db	623	AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGAAGTGCANGAAACAAGACCTA	682

QY 361 CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTTG 420
 ||| ||||| || ||| ||| ||||| | | | | | ||||| || | |||||
 Db 683 CAGAATGTANGAGGAGCCTNCCACGGAGCAGAANATGCCACATCACCGCANGATCCTTTG 742
 QY 421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATT 479
 || | ||||| | ||||| ||||| || | | | | |||
 Db 743 CTGCTTGAGCAACCTGCANAACATCGAAACACCTACCAAATAACATNTATAAGTCCAAT 801

RESULT 7

BF383724

LOCUS BF383724 594 bp mRNA linear EST 27-NOV-2000

DEFINITION 602044632F1 NCI_CGAP_Li9 Mus musculus cDNA clone IMAGE:4194295 5', mRNA sequence.

ACCESSION BF383724

VERSION BF383724.1 GI:11365029

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 594)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM9527 row: p column: 08

High quality sequence stop: 589.

FEATURES

source

Location/Qualifiers

1..594

/organism="Mus musculus"

/mol_type="mRNA"

/strain="FVB/N"

/db_xref="taxon:10090"

/clone="IMAGE:4194295"

/lab_host="DH10B (T1 phage-resistant)"

/clone_lib="NCI_CGAP_Li9"

/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;

Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 1.9 kb. Constructed by Life

Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 175 a 162 c 142 g 115 t

ORIGIN

Query Match 64.0%; Score 334.8; DB 10; Length 594;

Best Local Similarity 82.0%; Pred. No. 2.9e-73;

Matches 400; Conservative 0; Mismatches 82; Indels 6; Gaps 1;

QY 16 TGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGACAGGGGCTTTTATTTTC 75

Db	107	TGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGACCGAGGGGCTTTTACTTC	166
Qy	76	AACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAGACAGGCATCGTGGAT	135
Db	167	AACAAGCCACAGGCTATGGCTCCAGCATTTCGGAGGGCACCTCAGACAGGCATTGTGGAT	226
Qy	136	GAGTGTCTGCTTCCGGAGCTGTGTATCTGAGGAGGCTGGAGATGTACTGTGCACCCCTCAAG	195
Db	227	GAGTGTCTGCTTCCGGAGCTGTGTATCTGAGGAGACTGGAGATGTACTGTGCCCCACTGAAG	286
Qy	196	CCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGACATGCCCAAGACTCAG	255
Db	287	CCTACAAAAGCAGCCCGCTCTATCCGTGCCCAGCGCCACACTGCATGCCCAAGACTCAG	346
Qy	256	AAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGGAGAAGGAAAGGAAGT	315
Db	347	AAGTCCCCGTCCCTATCGACAAAACAAGAAAACGAAGCTGCAAAGGAGAAGGAAAGGAAGT	406
Qy	316	ACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTACAGGATGTAGGAAGA	375
Db	407	ACATTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTACAGAATGTAGGAGGA	466
Qy	376	CCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTTGCTCTGCACAGTTACC	435
Db	467	GCCTCCACGAGCAGAAAAATGCCACATCACCGCAGGATCCTTTGCTGCTTGAGCAACCT	526
Qy	436	TGTAAACATTGGAATACCGGCCA-----AAAAATAAGTTTGATCACATTTCAAAGATGG	489
Db	527	GCAAAACATCGAAACACCTACCAAATAACAATAATAAGTCCAATAACATTACAAAGATGG	586
Qy	490	CATTTCCC	497
Db	587	GCATTGCC	594

cdNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: NDAM371 row: p column: 18
 High quality sequence stop: 707.

FEATURES
 source Location/Qualifiers
 1. .796
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:30341081"
 /tissue_type="Human Placenta"
 /lab_host="DH10B TonA"
 /clone_lib="NIH_MGC_147"
 /note="Organ: placenta; Vector: pBluescriptR; Site_1:
 all-XhoI; Site_2: BamH; Oligo-dT primed using primer
 5'-TTTTTTTTTTTTTTVN-3', size-selected for average
 insert size 2.3 kb and normalized to ROT 5. This is a
 primary library enriched for full-length clones and
 constructed using the Cap-trapper method (Carninci, in
 preparation). Library constructed by M. Brownstein
 (NIMH/NHGRI, National Institutes of Health). Note: This is
 a NIH_MGC library."

BASE COUNT 224 a 197 c 191 g 184 t
 ORIGIN

Query Match 63.9%; Score 334.4; DB 14; Length 796;
 Best Local Similarity 84.6%; Pred. No. 3.9e-73;
 Matches 445; Conservative 0; Mismatches 26; Indels 55; Gaps 4;

```

Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
      |||
Db      180 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 239
      |||

Qy      61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGGCACCTCAG 120
      |||
Db      240 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 299
      |||

Qy      121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
      |||
Db      300 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 359
      |||

Qy      181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240
      |||
Db      360 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC 419
      |||

Qy      241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
      |||
Db      420 ATGCCCAAGACCCAG----- 434
      |||

Qy      301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
      |||
Db      435 -----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 487
      |||

Qy      361 CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTTG 420
      |||

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      |||
Db      488 CAGGATGTAGGAAGACCCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG 547
      |||
Qy      421 CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACAT 478
      |||
Db      548 CTCTGCACGAGTTACCTGTAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACAT 607
      |||
Qy      479 TTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTTC 523
      |||
Db      608 TTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTTC 653

```

RESULT 9

AW495481/c

LOCUS AW495481 499 bp mRNA linear EST 24-FEB-2000

DEFINITION UI-M-BH3-ay-g-11-0-UI.s1 NIH_BMAP_M_S4 Mus musculus cDNA clone
UI-M-BH3-ay-g-11-0-UI 3', mRNA sequence.

ACCESSION AW495481

VERSION AW495481.1 GI:7065762

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 499)

AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene
discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)

MEDLINE 97044477

PUBMED 8889548

COMMENT Contact: Chin, H

National Institute of Mental Health

6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA

Tel: 301 443 1706

Fax: 301 443 9890

Email: mEST@mail.nih.gov

The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. The sequence tag present in the cDNA between the NotI site
and the oligo-dT track served to identify it as a clone from the
normalized pineal glands library cDNA Library Preparation: M.B.
Soares Lab Clone distribution: Researchers may obtain BMAP cDNA
clones from RESEARCH GENETICS. It should be noted that Bento Soares
is generating a small number of additional specialized
non-redundant arrays of BMAP cDNAs whose availability will be
considered under appropriate and limited collaborative arrangements
Seq primer: M13 Forward
POLYA=Yes.

FEATURES

source

Location/Qualifiers

1. .499

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

```

/clone="UI-M-BH3-auy-g-11-0-UI"
/dev_stage="27-32 days"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NIH_BMAP_M_S4"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The
NIH_BMAP_M_S4 library is a subtracted library of a series,
ultimately derived from a mixture of individually tagged
normalized libraries from ten regions of the mouse brain
(cerebellum, brain stems, olfactory bulbs, hypothalamus,
cortex, amygdala, basal ganglia, pineal gland, striatum,
hippocampus) after a series of subtractions to reduce the
representation of cDNAs from which ESTs had already been
generated. The following serially subtracted libraries
were generated in this process: NIH_BMAP_M_S4,
NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, NIH_BMAP_M_S3.1,
NIH_BMAP_M_S2, NIH_BMAP_M_S1. The subtracted library
(NIH_BMAP_M_S4) was constructed as follows: PCR amplified
cDNA inserts from NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, and
NIH_BMAP_M_S3.1 clones from which 3' ESTs had been derived
was used as a driver in a hybridization with a pool of
the NIH_BMAP_M_S3.3, NIH_BMAP_M_S3.2, and NIH_BMAP_M_S3.1
libraries in the form of single-stranded circles. The
remaining single-stranded circles (subtracted library)
was purified by hydroxyapatite column chromatography,
converted to double-stranded circles and electroporated
into DH10B bacteria (LifeTechnologies) to generate the
NIH_BMAP_M_S4 library. This procedure has been previously
described (Bonaldo, Lennon and Soares, Genome Research
6:791-806, 1996)
TAG_LIB=NIH_BMAP_M_S4
TAG_TISSUE=pineal-glands
TAG_SEQ=CAGAC"

```

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BASE COUNT      86 a      112 c      124 g      177 t
ORIGIN

```

```

Query Match          61.6%; Score 322.2; DB 9; Length 499;
Best Local Similarity 82.3%; Pred. No. 4e-70;
Matches 396; Conservative 0; Mismatches 78; Indels 7; Gaps 2;

```

```

Qy      50 TGTGTGGAGACAGGGGCTTTTATTTCACAAGCCACAGGATACGGCTCCAGCAGTCGGA 109
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      499 TGTGTGGACCGAGGGGCTTTTACTTCAACAAGCCACAGGCTATGGCTCCAGCATTTCGGA 440

Qy      110 GGGCACCTCAGACAGGCATCGTGGATGAGTGCTTGCTTCCGGAGCTGTGATCTGAGGAGGC 169
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      439 GGGCACCTCAGACAGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGAC 380

Qy      170 TGGAGATGTACTGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGC 229
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      379 TGGAGATGTACTGTGCCCCACTGAAGCCTACAAAAGCAGCCCGCTCTATCCGTGCCCAGC 320

Qy      230 GCCACACCGACATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGA 289
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      319 GCCCACTGACATGCCCAAGACTCAGAAGTCCCCGTCCCTATCGACAAACAAGAAAACGA 260

Qy      290 AGTCTCAGAGGAGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGA 349

```

Db	259	AGCTGCAAAGGAGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGAAGTGCAGGA	200
Qy	350	AACAAGAACTACAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGC	409
Db	199	AACAAGACCTACAGAATGTAGGAGGAGCCTCCACGGAGCAGAAAAATGCCACATCACCGC	140
Qy	410	AGGACCCCTTTGCTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA-----AAAAA	463
Db	139	AGGATCCTTTGCTGCTTGAGCAACCTGCAAAACATCGAAACACCTACCAAATAACAATAA	80
Qy	464	TAAGTTTGATCACATTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATT	522
Db	79	TAAGTCCAATAACATTACAAAGATGGGCATTTCCCCCAATGAAATATACAAGTAAACATT	20
Qy	523	C 523	
Db	19	C 19	

AI876493/c

AI876493

642 bp

mRNA

linear

EST 21-JUL-1999

DEFINITION

IMAGE:1924219 3' similar to gb:X57025_rnal INSULIN-LIKE GROWTH FACTOR IA PRECURSOR (HUMAN); gb:X04482 Mouse mRNA for preproinsulin-like growth factor IB (MOUSE);, mRNA sequence.

AI876493

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 642)

AUTHORS

TITLE

The WashU-NCI Mouse EST Project 1999

JOURNAL

Unpublished

COMMENT

Contact: Marra M/WashU-NCI Mouse EST Project 1999

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

MGI : 980511

Seq primer: custom primer used

High quality sequence stop: 257.

FEATURES

Location/Qualifiers

source

1. 642.

```
/organism="Mus musculus"
```

```
/mol type="mRNA"
```


Db 83 CTGCTTGAGCAACCTGCAAAACATCGAAACACCTACCAAATAACAATAATAAGTCCAATA 24

QY 475 ACATTTCAAAGATGGCATTTCCTCC 497

Db 23 ACATTACAAAGATGGGCATTTCCTCC 1

RESULT 11

BM984670/c

LOCUS BM984670 673 bp mRNA linear EST 20-FEB-2003

DEFINITION UI-CF-EC1-abj-k-24-0-UI.s1 UI-CF-EC1 Homo sapiens cDNA clone
UI-CF-EC1-abj-k-24-0-UI 3', mRNA sequence.

ACCESSION BM984670

VERSION BM984670.1 GI:19610417

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 673)

AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene
discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)

MEDLINE 97044477

PUBMED 8889548

COMMENT Contact: McCray, PB

McCray Lab

University of Iowa

2024 University of Iowa Med Labs, Iowa City, IA 52242, USA

Tel: 319 356 4866

Fax: 319 356 7171

Email: paul-mccray@uiowa.edu

Tissue Procurement: Dr. M. J. Welsh, University of Iowa

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems

(www.openbiosystems.com).

Seq primer: M13 FORWARD

POLYA=Yes.

FEATURES

source

Location/Qualifiers

1..673

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="UI-CF-EC1-abj-k-24-0-UI"

/tissue_type="Lung"

/dev_stage="Adult and Fetal"

/lab_host="DH10B (Life Technologies) (T1 phage resistant)"

/clone_lib="UI-CF-EC1"

/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-CF-EC1 is a normalized cDNA library containing the
following tissue(s): Normal lung from adult and from fetal
day 64, day 87, week 19 and week 42. The library was

constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AAGTGCTTAC.

TAG_LIB=UI-CF-EC1

TAG_TISSUE=Normal Lung Epithelial Cells Tissue nos 369-371 and 380-383

TAG_SEQ=AAGTGCTTAC"

BASE COUNT 152 a 164 c 169 g 188 t
ORIGIN

Query Match 61.3%; Score 320.8; DB 12; Length 673;
Best Local Similarity 84.2%; Pred. No. 9.7e-70;
Matches 443; Conservative 0; Mismatches 27; Indels 56; Gaps 5;

```

Qy      1  GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
      |||
Db      492 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 433

Qy      61  AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
      |||
Db      432 AGGGG-TTTTATTTCAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 374

Qy      121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
      |||
Db      373 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 314

Qy      181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240
      |||
Db      313 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC 254

Qy      241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
      |||
Db      253 ATGCCCAAGACCCAG----- 239

Qy      301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
      |||
Db      238 -----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 186

Qy      361 CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTTG 420
      |||
Db      185 CAGGATGTAGGAAGACCCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG 126

Qy      421 CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACAT 478
      |||
Db      125 CTCTGCACGAGTTACCTGTAAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACAT 66

Qy      479 TTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTTC 523
      |||
Db      65  TTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTTC 20

```

RESULT 12

AI248089/c

LOCUS AI248089 575 bp mRNA linear EST 01-DEC-1998

DEFINITION qh69f05.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA
clone IMAGE:1849953 3' similar to gb:X57025_rnal INSULIN-LIKE
GROWTH FACTOR IA PRECURSOR (HUMAN);, mRNA sequence.

ACCESSION AI248089

VERSION AI248089.1 GI:3843486

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 575)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL Unpublished

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.govThis clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 918 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 380.

FEATURES

source

Location/Qualifiers

1..575

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:1849953"

/sex="male"

/dev_stage="20 week-post conception fetus"

/lab_host="DH10B (ampicillin resistant)"

/clone_lib="Soares_fetal_liver_spleen_1NFLS_S1"

/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)

with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;

This is a subtracted version of the original Soares fetal

liver spleen 1NFLS library. 1st strand cDNA was primed

with a Pac I - oligo(dT) primer [5'

AACTGGAAGAATTAATTAAAGATCTTTTTTTTTTTTTTTTTTTT 3'],

double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Pac I and cloned into the Pac I

and Eco RI sites of the modified pT7T3 vector. Library

went through one round of normalization. Library

constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT 135 a 152 c 131 g 156 t 1 others

ORIGIN

Query Match 60.6%; Score 316.8; DB 9; Length 575;

Best Local Similarity 83.8%; Pred. No. 9.4e-69;

Matches 428; Conservative 0; Mismatches 28; Indels 55; Gaps 4;

Qy 16 TGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGACAGGGGCTTTTATTTTC 75

||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

Db 551 TGCGGGGCTGAGCTGGTGNATGCTCTTCAGTTCGTGTGTGAAGACAGGGGCTTTTATTTTC 492

Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
Seq primer: M13-21.

FEATURES Location/Qualifiers
 source 1. .468
 /organism="Rattus sp."
 /mol_type="mRNA"
 /db_xref="ATCC (inhost):2027570"
 /db_xref="taxon:10118"
 /clone="RLIAT07"
 /clone_lib="Normalized rat liver, Bento Soares"
 /note="Organ: liver; Vector: pT7T3Pac; Site_1: EcoRI;
 Site_2: NotI"

BASE COUNT 85 a 115 c 119 g 149 t
ORIGIN

Query Match 59.1%; Score 309.2; DB 9; Length 468;
Best Local Similarity 81.8%; Pred. No. 7.2e-67;
Matches 383; Conservative 0; Mismatches 78; Indels 7; Gaps 2;

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Qy      63 GGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAGAC 122
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Db      468 GGGCTTTTACTTCAACAAGCCACAGGCTATGGCTCCAGCATTTCGGAGGGCACCACAGAC 409

Qy      123 AGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTACTG 182
      |||
Db      408 GGGCATTGTGGATGAGTGTGCTCCCGGAGCTGTGATCTGAGGAGGTTGGAGATGTACTG 349

Qy      183 TGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGACAT 242
      |||
Db      348 TGCTCCGCTGAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCAGCGCCACACTGACAT 289

Qy      243 GCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGGAG 302
      |||
Db      288 GCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGGAG 229

Qy      303 AAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGAGGAAACAAGAACTACA 362
      |||
Db      228 AAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGAGGAAACAAGACCTACA 169

Qy      363 GGATGTAGGAAGACCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTGCT 422
      |||
Db      168 GAATGTAGGAGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTGCT 109

Qy      423 CTGCACAGTTACCTGTAAACATTGGAATACCGGCCA-----AAAAATAAGTTTGATCAC 476
      |||
Db      108 GCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATACC 49

Qy      477 ATTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTTC 523
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Db      48 ATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTTC 1
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RESULT 14
AA542914/c
LOCUS AA542914 : 498 bp mRNA linear EST 19-AUG-1997

Qy 60 CAGGGGCTTTTATTTCACAAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCA 119
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 Db 416 CAGGGGC-TTTATTTCACAAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCA 358
 Qy 120 GACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTA 179
 |||
 Db 357 GACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTA 298
 Qy 180 CTGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGA 239
 ||
 Db 297 TTGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGA 238
 Qy 240 CATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAG 299
 |||
 Db 237 CATGCCCAAGACCCAG----- 222
 Qy 300 GAGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACT 359
 |||
 Db 221 -----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACT 170
 Qy 360 ACAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTT 419
 |||
 Db 169 ACAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTT 110
 Qy 420 GCTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACA 477
 |||
 Db 109 GCTCTGCACGAGTTACCTGTAAACTTTGGAACACCTACCAAAAAAATAAGTTTGATAACA 50
 Qy 478 TTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
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 Db 49 TTTAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTC 3

RESULT 15

AI604642

LOCUS AI604642 882 bp mRNA linear EST 21-APR-1999

DEFINITION vm43d08.y1 Stratagene mouse diaphragm (#937303) Mus musculus cDNA clone IMAGE:1001007 5' similar to gb:M11568 INSULIN-LIKE GROWTH FACTOR IB PRECURSOR (HUMAN); gb:X04482 Mouse mRNA for preproinsulin-like growth factor IB (MOUSE);, mRNA sequence.

ACCESSION AI604642

VERSION AI604642.1 GI:4613809

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 882)

AUTHORS Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.

TITLE The WashU-NCI Mouse EST Project 1999

JOURNAL Unpublished

COMMENT Contact: Marra M/WashU-NCI Mouse EST Project 1999
 Washington University School of Medicine

DEFINITION ni98c10.s1 NCI_CGAP_Pr21 Homo sapiens cDNA clone IMAGE:984882 3' similar to gb:X57025_rnal INSULIN-LIKE GROWTH FACTOR IA PRECURSOR (HUMAN);, mRNA sequence.

ACCESSION AA542914

VERSION AA542914.1 GI:2291394

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 498)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 603 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 412.

FEATURES

source Location/Qualifiers

1..498

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:984882"

/sex="male"

/tissue_type="normal prostate"

/lab_host="DH10B"

/clone_lib="NCI_CGAP_Pr21"

/note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from normal prostate bulk tissue, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is not normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "

BASE COUNT 105 a 135 c 123 g 135 t

ORIGIN

Query Match 58.3%; Score 305; DB 9; Length 498;

Best Local Similarity 83.5%; Pred. No. 8.2e-66;

Matches 440; Conservative 0; Mismatches 30; Indels 57; Gaps 6;

Qy 1 GGACCGGAGACGCTCTGCGGTGC-TGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGA 59

|||||||

Db 476 GGACCGGAGAACTTTTGGCGGGCTTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGA 417

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:565223

This read is a RESEQUENCE of a previously sequenced mouse clone

This read has been verified (found to hit its original self in the
correct orientation)

Seq primer: -40RP from Gibco

High quality sequence stop: 361.

FEATURES

source

Location/Qualifiers

1. .882

/organism="Mus musculus"

/mol_type="mRNA"

/db_xref="taxon:10090"

/clone="IMAGE:1001007"

/tissue_type="diaphragm"

/dev_stage="adult"

/lab_host="SOLR (kanamycin resistant)"

/clone_lib="Stratagene mouse diaphragm (#937303)"

/note="Organ: diaphragm; Vector: pBluescript SK-; Site_1:

EcoRI; Site_2: XhoI; Cloned unidirectionally from mRNA

prepared from diaphragm muscle. Primer: Oligo dT. Average

insert size: 1.5 kb. Uni-ZAP XR Vector; ~5' adaptor

sequence: 5' GAATTCGGCACGAG 3' ~3' adaptor sequence: 5'

CTCGAGTTTTTTTTTTTTTTTTTTT 3'"

BASE COUNT

236 a 226 c 183 g 223 t 14 others

ORIGIN

Query Match 57.2%; Score 299; DB 9; Length 882;

Best Local Similarity 77.2%; Pred. No. 3e-64;

Matches 393; Conservative 0; Mismatches 109; Indels 7; Gaps 3;

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Db      377 GGACCAGAGACCCTTTGCGGNGCTGAGCTGNTGGATGCTCTTCAGTTCGTGTGTGGACCG 436

Qy      61 AGGGGCTTTTATTTCAACAAGCCCAAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      437 AGGGGCTTTTACTTCAACAAGCCCAAGGCTATGGCTCCAGCATTTTCGAGGGCACCTCAG 496

Qy      121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      497 ACAGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGANGAGACTGGAGATGTAC 556

Qy      181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      557 TGTGCCCCACTGAAGCCTACANAAGCAGCCCGCTCTATCCGTGCCAGCGCCACACTGAC 616

Qy      241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      617 ATGCNNCAGACTCAGAAGTCCCCGTNCCTATCGACNNAACAGAAAACGAAGCTTGCAAGG 676

Qy      301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAATA 360
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```

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Db      677 GAGAGGGAAGGGAGTACATTTGAGGAACACANGTNGAGGAAGTGCANGAAACAAGACCTA 736
Qy      361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
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Db      737 CCAGATGTANGAGGAGCCTTC--AACCGAGCAGAAATGCACATCACCCGNAGATCCTTTG 794
Qy      421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAA---AAAATAAGTTTGATCAC 476
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Db      795 CT-GCTTGAGCTAACTGCAAACATCGAACCACCTTACCAATTACAATAATAAGTTCAATAA 853
Qy      477 ATTTCAAAGATGGCATTTCCTCCCAATGAA 505
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Db      854 CATACAAAGATGGCATTTCCTCCCAATGAA 882

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Search completed: December 13, 2003, 07:29:51
Job time : 1704.81 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 13, 2003, 05:41:20 ; Search time 2336.77 Seconds
(without alignments)
9156.102 Million cell updates/sec

Title: US-09-852-261-5
Perfect score: 523
Sequence: 1 ggaccggagacgctctgcgg.....aaatacacaagtaaaccattc 523

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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 35: em_htg_rod:*
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 39: em_htgo_hum:*
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 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	523	100.0	523	6	AX147746	AX147746 Sequence
2	523	100.0	523	6	AX300783	AX300783 Sequence
3	467.4	89.4	517	6	AX147742	AX147742 Sequence
4	467.4	89.4	517	6	AX300779	AX300779 Sequence
5	409	78.2	471	6	AX147754	AX147754 Sequence
6	409	78.2	471	6	AX300791	AX300791 Sequence
7	364.8	69.8	1536	10	BC012409	BC012409 Mus muscu
8	361.6	69.1	798	10	RNIGFI2	X06108 Rat mRNA (c
9	361.6	69.1	958	10	RNIGFI1	X06107 Rat mRNA (c
10	358.4	68.5	710	10	RATIGFIA	M15480 Rat insulin
11	356.8	68.2	539	6	AX147744	AX147744 Sequence
12	356.8	68.2	539	6	AX300781	AX300781 Sequence
13	349.4	66.8	651	10	MMIGFIBR	X04482 Mouse mRNA
14	336	64.2	432	4	AF022961	AF022961 Oryctolag
15	334.4	63.9	7260	6	AX375028	AX375028 Sequence
16	334.4	63.9	7260	6	AX411095	AX411095 Sequence
17	334.4	63.9	7260	9	HSIGFACI	X57025 Human IGF-I
18	332.8	63.6	666	6	A29119	A29119 H.sapiens I
19	332.8	63.6	725	9	HSIGFI	X00173 Homo sapien
20	332.8	63.6	728	9	HUMGFII	M29644 Human insul
21	332.4	63.6	616	9	HSIGF1A	X56773 H.sapiens m
22	331.2	63.3	620	6	I08370	I08370 Sequence 2
23	331.2	63.3	1076	9	HUMIGFI	M27544 Human insul
24	316.8	60.6	444	9	HSU40870	U40870 Human alter
25	293.8	56.2	532	4	SSIIGF1M	X17492 Porcine mRN
26	293.8	56.2	567	4	PIGGFIIA	M31175 Pig insulin
27	286.2	54.7	888	4	ECU85272	U85272 Equus cabal
28	281.8	53.9	978	4	GOTIGFI	D11378 Goat mRNA f
29	281.8	53.9	978	6	E05279	E05279 DNA encodin
30	280.2	53.6	1284	4	BTILGF1A	X15726 Bovine mRNA
31	275.4	52.7	747	4	SHPIGFIA6	M31735 Sheep insul
32	275.4	52.7	790	4	SHPIGFIA21	M31734 Sheep insul
33	275.4	52.7	1015	4	SHPIGFIA46	M31736 Sheep insul

34	275.4	52.7	1107	4	SHPIGFIA1	M30653 Sheep insul
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36	275.2	52.6	1094	9	HUMGF1B	M11568 Human insul
37	275.2	52.6	1136	6	E01349	E01349 cDNA encodi
38	275.2	52.6	1136	6	I08009	I08009 Sequence 3
39	274.6	52.5	3599	6	BD063790	BD063790 Insulin-l
40	274.6	52.5	3599	6	BD069041	BD069041 Treatment
41	274.6	52.5	3600	6	BD063789	BD063789 Insulin-l
42	274.6	52.5	3600	6	BD069040	BD069040 Treatment
43	273.6	52.3	612	9	HUMIGF1B	M37484 Human insul
44	271.6	51.9	696	10	MMIGFIAR	X04480 Mouse mRNA
45	268.4	51.3	513	26	RNMGJIL	M17714 Rat insulin

ALIGNMENTS

RESULT 1

AX147746

LOCUS AX147746 523 bp DNA linear PAT 31-AUG-2001

DEFINITION Sequence 5 from Patent WO0136483.

ACCESSION AX147746

VERSION AX147746.1 GI:14346791

KEYWORDS

SOURCE Oryctolagus cuniculus (rabbit)

ORGANISM Oryctolagus cuniculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

REFERENCE 1

AUTHORS Goldspink, G.R. and Johnson, I.R.

TITLE Use of the insulin-like-growth factor i isoform mgf for the
treatment of neurological disorders

JOURNAL Patent: WO 0136483-A 5 25-MAY-2001;

University College London (GB)

FEATURES Location/Qualifiers

source

1..523

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/db_xref="taxon:9986"

CDS

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/translation="GPETLCGAELVDALQFVCGDRGFYFNKPTGYGSSRRAPQTGIV

DECCFRSCDLRRLEMYCAPLKPAAKARSVRAQRHTDMPKTQKYQPPSTNKKMKSQRRR

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BASE COUNT 154 a 129 c 142 g 98 t

ORIGIN

Query Match 100.0%; Score 523; DB 6; Length 523;

Best Local Similarity 100.0%; Pred. No. 9.5e-150;

Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360

Qy 361 CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
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Db 361 CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420

Qy 421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480
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Qy 481 CAAAGATGGCATTTCGCCCAATGAAATACACAAGTAAACATTC 523
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Db 481 CAAAGATGGCATTTCGCCCAATGAAATACACAAGTAAACATTC 523

RESULT 2

AX300783

LOCUS AX300783 523 bp DNA linear PAT 30-NOV-2001

DEFINITION Sequence 5 from Patent WO0185781.

ACCESSION AX300783

VERSION AX300783.1 GI:17382064

KEYWORDS

SOURCE Oryctolagus cuniculus (rabbit)

ORGANISM Oryctolagus cuniculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

REFERENCE 1

AUTHORS Goldspink, G.D. and Terenghi, G.B.

TITLE Repair of nerve damage

JOURNAL Patent: WO 0185781-A 5 15-NOV-2001;
 University College London (GB) ; East Grinstead Medical Research
 Trust (GB)

FEATURES

source Location/Qualifiers
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 /organism="Oryctolagus cuniculus"
 /mol_type="genomic DNA"
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CDS

<1. .336
/note="unnamed protein product"
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/db_xref="GI:17382065"
/translation="GPETLCGAELVDALQFVCGDRGFYFNKPTGYGSSRRAPQTGIV
DECCFRSCDLRRLEMYCAPLKPAAARSVRAQRHTDMPKTQKYQPPSTNKKMKSQRRR
KGSTFEEHK"

BASE COUNT 154 a 129 c 142 g 98 t
ORIGIN

Query Match 100.0%; Score 523; DB 6; Length 523;
Best Local Similarity 100.0%; Pred. No. 9.5e-150;
Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
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Qy     61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
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Qy    121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
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Db    121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

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Db    181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240

Qy    241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
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Db    241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300

Qy    301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
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Db    301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360

Qy    361 CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTG 420
      |||
Db    361 CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTG 420

Qy    421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480
      |||
Db    421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480

Qy    481 CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACATTC 523
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Db    481 CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACATTC 523
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RESULT 3

AX147742

LOCUS AX147742 517 bp DNA linear PAT 31-AUG-2001
DEFINITION Sequence 1 from Patent WO0136483.
ACCESSION AX147742

VERSION AX147742.1 GI:14346787
 KEYWORDS .
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Goldspink, G.R. and Johnson, I.R.
 TITLE Use of the insulin-like-growth factor i isoform mgf for the
 treatment of neurological disorders
 JOURNAL Patent: WO 0136483-A 1 25-MAY-2001;
 University College London (GB)
 FEATURES Location/Qualifiers
 source 1..517
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 CDS <1..333
 /note="unnamed protein product"
 /codon_start=1
 /protein_id="CAC41175.1"
 /db_xref="GI:14346788"
 /db_xref="REMTREMBL:CAC41175"
 /translation="GPETLCGAELVDALQFVCGDRGFYFNKPTGYGSSSRRAPQTGIV
 DECCFRSCDLRRLEMYCAPLKPASARSVRAQRHTDMPKTQKYQPPSTNKNTKSQRRK
 GSTFEEHK"
 BASE COUNT 150 a 130 c 139 g 98 t
 ORIGIN

Query Match 89.4%; Score 467.4; DB 6; Length 517;
 Best Local Similarity 96.2%; Pred. No. 1.3e-132;
 Matches 501; Conservative 0; Mismatches 16; Indels 4; Gaps 2;

Qy 1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
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 Db 1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
 Qy 61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
 |||||
 Db 61 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120
 Qy 121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
 |||||
 Db 121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
 Qy 181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
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 Db 181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 240
 Qy 241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
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 Db 241 ATGCCCAAGACCCAGAAGTATCAGCCCCATCTACCAACAAGAACACGAAGTCTCA---G 297
 Qy 301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
 |||||
 Db 298 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 357

Qy 361 CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
 |||||
 Db 358 CAGGATGTA-GAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 416
 Qy 421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480
 |||||
 Db 417 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 476
 Qy 481 CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACAT 521
 |||||
 Db 477 CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACAT 517

RESULT 4

AX300779

LOCUS AX300779 517 bp DNA linear PAT 30-NOV-2001

DEFINITION Sequence 1 from Patent WO0185781.

ACCESSION AX300779

VERSION AX300779.1 GI:17382060

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Goldspink, G.D. and Terenghi, G.B.

TITLE Repair of nerve damage

JOURNAL Patent: WO 0185781-A 1 15-NOV-2001;
 University College London (GB) ; East Grinstead Medical Research
 Trust (GB)

FEATURES Location/Qualifiers

source

1. 517

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

CDS

<1. 333

/note="unnamed protein product"

/codon_start=1

/protein_id="CAD13040.1"

/db_xref="GI:17382061"

/translation="GPETLCGAE LVDALQFVCGDRGFYFNKPTGYGSSSRAPQTGIV
 DECCFRSCDLRRLEMYCAPLKPASRSVRAQRHTDMPKTQKYQPPSTNKNTKSQRRK
 GSTFEEHK"

BASE COUNT 150 a 130 c 139 g 98 t

ORIGIN

Query Match 89.4%; Score 467.4; DB 6; Length 517;

Best Local Similarity 96.2%; Pred. No. 1.3e-132;

Matches 501; Conservative 0; Mismatches 16; Indels 4; Gaps 2;

Qy 1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
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Db 1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

Qy 61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
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Db 61 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCTCAG 120

Qy 121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
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 Db 121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180
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 Qy 181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
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 Db 181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 240
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 Qy 241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
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 Db 241 ATGCCCAAGACCCAGAAGTATCAGCCCCATCTACCAACAAGAACACGAAGTCTCA---G 297
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 Qy 301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
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 Db 298 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 357
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 Qy 361 CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTTG 420
 |||||
 Db 358 CAGGATGTA-GAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTTG 416
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 Qy 421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGTATCACATTT 480
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 Db 417 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGTATCACATTT 476
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 Qy 481 CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACAT 521
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 Db 477 CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACAT 517
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RESULT 5

AX147754

LOCUS AX147754 471 bp DNA linear PAT 08-JUN-2001

DEFINITION Sequence 13 from Patent WO0136483.

ACCESSION AX147754

VERSION AX147754.1 GI:14348552

KEYWORDS

SOURCE Oryctolagus cuniculus (rabbit)

ORGANISM Oryctolagus cuniculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

REFERENCE 1

AUTHORS Goldspink, G.R. and Johnson, I.R.

TITLE Use of the insulin-like-growth factor i isoform mgf for the
 treatment of neurological disorders

JOURNAL Patent: WO 0136483-A 13 25-MAY-2001;
 University College London (GB)

FEATURES Location/Qualifiers

source 1..471
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 /mol_type="genomic DNA"
 /db_xref="taxon:9986"
 CDS <1..318
 /note="unnamed protein product"
 /codon_start=1
 /protein_id="CAC41264.1"
 /db_xref="GI:14348553"

/translation="GPETLCGAELVDALQFVCGDRGFYFNKPTGYGSSSSRRAPQTGIV
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YRM"

BASE COUNT 132 a 118 c 131 g 90 t
ORIGIN

Query Match 78.2%; Score 409; DB 6; Length 471;
Best Local Similarity 90.1%; Pred. No. 1.3e-114;
Matches 471; Conservative 0; Mismatches 0; Indels 52; Gaps 1;

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Qy     61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
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Db     61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120

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Db    121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy    181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240
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Db    181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240

Qy    241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
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Db    241 ATGCCCAAGACTCAG----- 255

Qy    301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
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Db    256 -----AAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 308

Qy    361 CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
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Db    309 CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 368

Qy    421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480
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Db    369 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 428

Qy    481 CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACATTTC 523
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Db    429 CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACATTTC 471
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RESULT 6

AX300791

LOCUS AX300791 471 bp DNA linear PAT 30-NOV-2001

DEFINITION Sequence 13 from Patent WO0185781.

ACCESSION AX300791

VERSION AX300791.1 GI:17382072

KEYWORDS

SOURCE Oryctolagus cuniculus (rabbit)

ORGANISM Oryctolagus cuniculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

REFERENCE 1

AUTHORS Goldspink, G.D. and Terenghi, G.B.

TITLE Repair of nerve damage

JOURNAL Patent: WO 0185781-A 13 15-NOV-2001;
University College London (GB) ; East Grinstead Medical Research
Trust (GB)

FEATURES Location/Qualifiers

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/db_xref="taxon:9986"

CDS <1. .318
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/codon_start=1
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YRM"

BASE COUNT 132 a 118 c 131 g 90 t

ORIGIN

Query Match 78.2%; Score 409; DB 6; Length 471;
Best Local Similarity 90.1%; Pred. No. 1.3e-114;
Matches 471; Conservative 0; Mismatches 0; Indels 52; Gaps 1;

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Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTTCGTGTGTGGAGAC 60
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Db      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTTCGTGTGTGGAGAC 60

Qy     61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
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Db    121 ACAGGCATCGTGGATGAGTGCTTGCTTCCGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy    181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGTCCGTCCGTGCCCAGCGCCACACCGAC 240
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Db    181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGTCCGTCCGTGCCCAGCGCCACACCGAC 240

Qy    241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
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Db    241 ATGCCCAAGACTCAG----- 255

Qy    301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
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Db    256 -----AAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 308

Qy    361 CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTTG 420
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Db    309 CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTTG 368

Qy    421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGTATCACATTT 480
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Db 369 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 428

QY 481 CAAAGATGGCATTTCCTCCAATGAAATACACAAGTAAACATTTC 523

Db 429 CAAAGATGGCATTTCCTCCAATGAAATACACAAGTAAACATTTC 471

RESULT 7

BC012409

LOCUS BC012409 1536 bp mRNA linear ROD 16-APR-2003

DEFINITION Mus musculus insulin-like growth factor 1, mRNA (cDNA clone MGC:18617 IMAGE:4194295), complete cds.

ACCESSION BC012409

VERSION BC012409.1 GI:15214568

KEYWORDS MGC.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 1536)

AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

MEDLINE 22388257

PUBMED 12477932

REFERENCE 2 (bases 1 to 1536)

AUTHORS Strausberg,R.

TITLE Direct Submission

JOURNAL Submitted (15-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT Contact: MGC help desk

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Baylor College of Medicine Human Genome

Sequencing Center

Center code: BCM-HGSC

Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>

Contact: amg@bcm.tmc.edu

Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAK Plate: 24 Row: k Column: 11

This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6754307.

FEATURES	Location/Qualifiers
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gene	1..1536 /gene="Igfl" /db_xref="LocusID:16000" /db_xref="MGI:96432"
CDS	28..429 /codon_start=1 /product="insulin-like growth factor 1" /protein_id="AAH12409.1" /db_xref="GI:15214569" /db_xref="LocusID:16000" /translation="MSSSHLFYLALCLLTFTSSTTAGPETLCGAELVDALQFVCGPRG FYFNKPTGYGSSIRRAPQTGIVDECCFRSCDLRRLEMYCAPLKPTKAARSIRAQRHTD MPKTQKSPSLSTNKKTKLQRRRKGSTFEEHK"
BASE COUNT	485 a 324 c 303 g 424 t
ORIGIN	

Query Match 69.8%; Score 364.8; DB 10; Length 1536;
Best Local Similarity 83.2%; Pred. No. 6.6e-101;
Matches 441; Conservative 0; Mismatches 82; Indels 7; Gaps 2;

Qy	1	GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC	60
Db	94	GGACCAGAGACCCCTTTGCGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGACCG	153
Qy	61	AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG	120
Db	154	AGGGGCTTTTACTTCAACAAGCCACAGGCTATGGCTCCAGCATTGGAGGGCACCTCAG	213
Qy	121	ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC	180
Db	214	ACAGGCATTGTGGATGAGTGTGCTTCCGGAGCTGTGATCTGAGGAGACTGGAGATGTAC	273
Qy	181	TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC	240


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BASE COUNT      238 a      196 c      183 g      181 t
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Best Local Similarity 82.8%;  Pred. No. 5.8e-100;
Matches 439;  Conservative 0;  Mismatches 84;  Indels 7;  Gaps 2;

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Db     217 GGACCAGAGACCCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 276

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Db     277 AGGGGCTTTTACTTCAACAAGCCCAAGGCTATGGCTCCAGCATTCCGAGGGCACCACAG 336

Qy     121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
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Db     337 ACGGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 396

Qy     181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
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Db     457 ATGCCCAAGACTCAGAAGTCCCAGCCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 516

Qy     301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
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Qy     361 CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTTG 420
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Db     577 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTACCGCAAGATCCTTTG 636

Qy     421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA-----AAAAATAAGTTTGATC 474
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Qy     475 ACATTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATT 523
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Db      523  ACGGGCATTGTGGATGAGTGTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 582
Qy      181  TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
Db      583  TGTGCTCCGCTGAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 642
Qy      241  ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
Db      643  ATGCCCAAGACTCAGAAGTCCCAGCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 702
Qy      301  AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
Db      703  AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 762
Qy      361  CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTTG 420
Db      763  CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTACCGCAAGATCCTTTG 822
Qy      421  CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA-----AAAAATAAGTTTGATC 474
Db      823  CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 882
Qy      475  ACATTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTTC 523
Db      883  CCATTTCAAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTTC 932

```

RESULT 10

RATIGFIA

LOCUS RATIGFIA 710 bp mRNA linear ROD 27-APR-1993

DEFINITION Rat insulin-like growth factor I (IGF-I) mRNA, complete cds.

ACCESSION M15480

VERSION M15480.1 GI:204749

KEYWORDS growth factor; insulin-like growth factor.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 710)

AUTHORS Roberts,C.T. Jr., Lasky,S.R., Lowe,W.L. Jr., Seaman,W.T. and
LeRoith,D.

TITLE Molecular cloning of rat insulin-like growth factor I complementary
deoxyribonucleic acids: differential messenger ribonucleic acid
processing and regulation by growth hormone in extrahepatic tissues

JOURNAL Mol. Endocrinol. 1 (3), 243-248 (1987)

MEDLINE 88288198

PUBMED 3453891

COMMENT Original source text: Rat (Sprague-Dawley) adult liver cDNA to
mRNA, clone pRIGF-1-42.

Draft entry and computer-readable copy of sequence in [Mol.
Endocrinol. (1987) In press] kindly


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provided by S.R.Lasky, 16-MAR-1987.
FEATURES
    source                1. .710
                          /organism="Rattus norvegicus"
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                          /db_xref="taxon:10116"
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                          /codon_start=1
                          /protein_id="AAA41385.1"
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                          /translation="MSSSHLFYLA LCLLTFTSSATAGPETL CGAELVDALQFVCGPRG
FYFNKPTGYGSSIRRAPQTGIVDECCFRSCDLRRLEMYCVRCKPTKSARSIRAQRHTD
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                          /product="insulin-like growth factor C peptide"
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                          /product="insulin-like growth factor A peptide"
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                          /product="insulin-like growth factor D peptide"
    mat_peptide           382. .504
                          /product="insulin-like growth factor E peptide"
BASE COUNT      202 a    191 c    172 g    145 t
ORIGIN          1 bp upstream of EcoRI site.

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Db      61 AGGGGCTTTTACTTCAACAAGCCACAGTCTATGGCTCCAGCATTTCGGAGGGCACCACAG 120
Qy      121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
Db      121 ACGGGCATTGTGGATGAGTGTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
Qy      181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
Db      181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240
Qy      241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
Db      241 ATGCCCAAGACTCAGAAGTCCCAGCCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300
Qy      301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
Db      301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360
Qy      361 CAGGATGTAGGAAGACCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTTG 420
Db      361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420
Qy      421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA-----AAAAATAAGTTTGTATC 474
Db      421 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 480
Qy      475 ACATTTCAAAGAT-GGCATTTCCTCCCAATGAAATACACAAGTAAACATTTC 523
Db      481 TCATTTCAGAGATGGGCATTTCCTCAATGAAATACACAAGTAAACATTTC 530

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RESULT 12

AX300781

LOCUS AX300781 539 bp DNA linear PAT 30-NOV-2001

DEFINITION Sequence 3 from Patent WO0185781.

ACCESSION AX300781

VERSION AX300781.1 GI:17382062

KEYWORDS

SOURCE Rattus sp.

ORGANISM Rattus sp.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1

AUTHORS Goldspink, G.D. and Terenghi, G.B.

TITLE Repair of nerve damage

JOURNAL Patent: WO 0185781-A 3 15-NOV-2001;
University College London (GB) ; East Grinstead Medical Research
Trust (GB)

FEATURES Location/Qualifiers

source 1..539

/organism="Rattus sp."

/mol_type="genomic DNA"

/db_xref="taxon:10118"

CDS <1..336

/note="unnamed protein product"

/codon_start=1
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/translation="GPETLCGAELVDALQFVCGPRGFYFNKPTVYGSSIRRAPQTGIV
DECCFRSCDLRRLEMYCVRCKPTKSARSIRAQRHTDMPKTQKSQPLSTHKRKLQRRR
KGSTLEEHK"

BASE COUNT 161 a 136 c 139 g 103 t
ORIGIN

Query Match 68.2%; Score 356.8; DB 6; Length 539;
Best Local Similarity 82.3%; Pred. No. 1.6e-98;
Matches 436; Conservative 0; Mismatches 87; Indels 7; Gaps 2;

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Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
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Db      1 GGACCAGAGACCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60

Qy     61 AGGGGCTTTTATTTCAACAAGCCCAAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
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Db     61 AGGGGCTTTTACTTCAACAAGCCCAAGTCTATGGCTCCAGCATTTCGGAGGGCACCACAG 120

Qy    121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
        || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    121 ACGGGCATTGTGGATGAGTGTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy    181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240
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Db    181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCAGCGCCACACTGAC 240

Qy    241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
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Qy    301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
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Db    301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360

Qy    361 CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
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Db    361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420

Qy    421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA-----AAAAATAAGTTTGATC 474
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Db    421 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 480

Qy    475 ACATTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTTC 523
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Db    481 TCATTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTTC 530
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RESULT 13

MMIGFIBR

LOCUS MMIGFIBR 651 bp mRNA linear ROD 21-MAR-1995

DEFINITION Mouse mRNA for preproinsulin-like growth factor IB.

ACCESSION X04482

VERSION X04482.1 GI:51806

KEYWORDS growth factor; insulin-like growth factor IB; preproinsulin-like

```

SOURCE      growth factor IB; signal peptide.
            Mus musculus (house mouse)
ORGANISM    Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1 (bases 1 to 651)
AUTHORS     Bell,G.I., Stempien,M.M., Fong,N.M. and Rall,L.B.
TITLE       Sequences of liver cDNAs encoding two different mouse insulin-like
            growth factor I precursors
JOURNAL      Nucleic Acids Res. 14 (20), 7873-7882 (1986)
MEDLINE     87040760
PUBMED      3774549

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FEATURES             Location/Qualifiers
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     CDS               73. .474
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     sig_peptide       73. .138
                        /note="signal peptide (aa -22 to -1)"
     mat_peptide       139. .348
                        /product="mature IGF-IB (aa 1-70)"
     misc_feature      349. .471
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Query Match 66.8%; Score 349.4; DB 10; Length 651;
Best Local Similarity 82.8%; Pred. No. 3.2e-96;
Matches 425; Conservative 0; Mismatches 81; Indels 7; Gaps 2;

QY 61 AGGGGCTTTTATTTCAACAAGCCCAAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
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 Db 199 AGGGGCTTTTACTTCAACAAGCCCAAGGCTATGGCTCCAGCATTTCGGAGGGCACCTCAG 258
 QY 121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
 |||||
 Db 259 ACAGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGACTGGAGATGTAC 318
 QY 181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240
 |||||
 Db 319 TGTGCCCCACTGAAGCCTACAAAAGCAGCCCGCTCTATCCGTGCCAGCGCCACACTGAC 378
 QY 241 ATGCCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
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 Db 379 ATGCCCCAAGACTCAGAAGTCCCCGTCCCTATCGACAAACAAGAAAACGAAGCTGCAAAGG 438
 QY 301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAATA 360
 |||||
 Db 439 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 498
 QY 361 CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTTG 420
 |||||
 Db 499 CAGAATGTAGGAGGAGCCTCCCAAGGAGCAGAAAATGCCACATCACCGCAGGATCCTTTG 558
 QY 421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA-----AAAAATAAGTTTGATC 474
 |||||
 Db 559 CTGCTTGAGCAACCTGCAAAACATCGAAACACCTACCAAATAACAATAATAAGTCCAATA 618
 QY 475 ACATTTCAAAGAT-GGCATTTCCCCCAATGAAA 506
 |||||
 Db 619 ACATTACAAAGATGGGCATTTCCCCCAATGAAA 651

RESULT 14

AF022961

LOCUS AF022961 432 bp mRNA linear MAM 14-OCT-1997

DEFINITION Oryctolagus cuniculus insulin-like growth factor IB (IGF-IB) mRNA, complete cds.

ACCESSION AF022961

VERSION AF022961.1 GI:2522201

KEYWORDS

SOURCE Oryctolagus cuniculus (rabbit)

ORGANISM Oryctolagus cuniculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

REFERENCE 1 (bases 1 to 432)

AUTHORS Flekna,G., Brem,G. and Mueller,M.

TITLE Direct Submission

JOURNAL Submitted (05-SEP-1997) Institute of Animal Breeding and Genetics, Veterinary University of Vienna, Veterinaerplatz 1, Vienna A-1210, Austria

FEATURES Location/Qualifiers

source

1..432

/organism="Oryctolagus cuniculus"

/mol_type="mRNA"

/strain="ZIKA hybrid strain"

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gene      1. .432
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CDS       1. .432
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        /protein_id="AAB80950.1"
        /db_xref="GI:2522202"
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BASE COUNT      105 a      126 c      115 g      86 t
ORIGIN

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Query Match          64.2%;  Score 336;  DB 4;  Length 432;
Best Local Similarity 100.0%;  Pred. No. 4.1e-92;
Matches 336;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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Qy     61  AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG  120
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Db    157  AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG  216

Qy    121  ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC  180
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Db    217  ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC  276

Qy    181  TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC  240
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Db    277  TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC  336

Qy    241  ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG  300
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Db    337  ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG  396

Qy    301  AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAG  336
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Db    397  AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAG  432

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RESULT 15

AX375028

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LOCUS      AX375028          7260 bp :   DNA       linear   PAT 01-MAR-2002
DEFINITION Sequence 31 from Patent WO0210436.
ACCESSION  AX375028
VERSION    AX375028.1  GI:19169860
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

REFERENCE 1
AUTHORS Baak,J. and Mutter,G.L.
TITLE Prognostic classification of breast cancer
JOURNAL Patent: WO 0210436-A 31 07-FEB-2002;
THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US) ; Baak, Jan (US)

FEATURES Location/Qualifiers
source 1. .7260
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

BASE COUNT 2330 a 1415 c 1240 g 2275 t
ORIGIN

Query Match 63.9%; Score 334.4; DB 6; Length 7260;
Best Local Similarity 84.6%; Pred. No. 2e-91;
Matches 445; Conservative 0; Mismatches 26; Indels 55; Gaps 4;

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Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
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Db    311 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 370

Qy      61 AGGGGCTTTTATTTCAACAAGCCCAAGGATACGGCTCCAGCAGTCGGAGGGGCACCTCAG 120
      |||
Db    371 AGGGGCTTTTATTTCAACAAGCCCAAGGGTATGGCTCCAGCAGTCGGAGGGGCGCCTCAG 430

Qy     121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
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Db    431 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 490

Qy     181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240
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Db    491 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC 550

Qy     241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
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Db    551 ATGCCCAAGACCCAG----- 565

Qy     301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
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Db    566 -----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 618

Qy     361 CAGGATGTAGGAAGACCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTTG 420
      |||
Db    619 CAGGATGTAGGAAGACCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG 678

Qy     421 CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACAT 478
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Db    679 CTCTGCACGAGTTACCTGTAACTTTGGAACACCTACCAAAAAAATAAGTTTGATAACAT 738

Qy     479 TTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATT 523
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Db    739 TTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATT 784

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GenCore version 5.1.6
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and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
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1	523	100.0	523	22	AAD06400		Rabbit IGF-I isofo
2	523	100.0	523	24	AAS16879		Rabbit mechano-gro
3	523	100.0	553	18	AAT84893		Rabbit insulin lik
4	467.4	89.4	517	22	AAD06398		Human IGF-I isofo
5	467.4	89.4	517	24	AAS16877		Human mechano-grow
6	409	78.2	471	22	AAD06405		Rabbit liver-type
7	409	78.2	471	24	AAS16884		Rabbit insulin-lik
8	356.8	68.2	539	22	AAD06399		Rat IGF-I isoform
9	356.8	68.2	539	24	AAS16878		Rat mechano-growth
10	349.4	66.8	651	25	ABV76185		Mouse insulin-like
11	334.4	63.9	818	8	AAN70436		Sequence encoding
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13	334.4	63.9	7260	24	ABK84583		Human cDNA differe
14	334.4	63.9	7260	24	ABN97244		Gene #3742 used to
15	334.4	63.9	7260	24	ABK64812		Human benign prost
16	334.4	63.9	7260	24	ABK35504		Human endometrial
17	334.4	63.9	7260	24	ABK35561		Gene IGF1 differen
18	332.8	63.6	777	18	AAT84894		Human insulin like
19	331.2	63.3	622	7	AAN60490		Human prepro-somat
20	281.8	53.9	978	14	AAQ47804		Sequence encoding
21	275.2	52.6	1136	8	AAN70435		Sequence encoding
22	274.6	52.5	3599	19	AAV50428		Plasmid pIG0552 lo
23	274.6	52.5	3599	19	AAV40796		Actual sequence of
24	274.6	52.5	3600	19	AAV50427		Plasmid pIG0552 up
25	274.6	52.5	3600	19	AAV40795		Expected sequence
26	274.6	52.5	5707	20	AAX88055		Plasmid pIG0335 DN
27	274.6	52.5	6345	20	AAX88054		Plasmid pIG0100A D
28	273.6	52.3	612	22	AAS14695		Human cDNA encodin
29	273.6	52.3	612	25	ABZ83309		Toxicologically re
30	266.8	51.0	1052	20	AAX27498		Rat liver form of
31	262	50.1	487	22	AAD06404		Rat liver-type IGF
32	262	50.1	487	24	AAS16883		Rat insulin-like g
33	250	47.8	671	24	ABT09479		Phase-1 Rat CT gen
34	237.6	45.4	317	24	AAS16882		Human insulin-like
35	237.6	45.4	318	22	AAD06403		Human liver-type I
36	237.6	45.4	462	19	AAV50426		Human IGF-1 encodi
37	237.6	45.4	462	19	AAV40794		Human IGF-I coding
38	237.6	45.4	462	24	ABZ35734		Human IGF1 polynuc
39	237.6	45.4	462	24	ABX09977		Human IGF1 DNA fra
40	237.6	45.4	462	24	ABV78158		Human IGF1 DNA SEQ
41	237.6	45.4	462	24	ABL91699		Human polynucleoti
42	209	40.0	286	25	ABV76186		Mouse insulin-like
43	193	36.9	210	24	AAD45568		Human insulin-like
44	193	36.9	210	24	AAD44955		Human insulin grow
45	193	36.9	210	24	ABA03146		Native mature IGF-

ALIGNMENTS

RESULT 1

AAD06400

ID AAD06400 standard; cDNA; 523 BP.

XX

AC AAD06400;

XX

DT 10-AUG-2001 (first entry)

XX

DE Rabbit IGF-I isoform mechano-growth factor (MGF) cDNA.

XX

KW Rabbit; IGF-I isoform; Insulin-like Growth Factor-I; MGF;
 KW mechano-growth factor; neurological disorder; neurodegenerative disorder;
 KW amyotrophic lateral sclerosis; spinal muscular atrophy; muscular atrophy;
 KW poliomyelitis; post-polio syndrome; toxin; motoneurone disorder;
 KW nerve damage; autosomal muscular dystrophy; diabetic neuropathy;
 KW sex-linked muscular dystrophy; peripheral neuropathy;
 KW Alzheimer's disease; Parkinson's disease; ss.

XX

OS Oryctolagus cuniculus.

XX

FH Key Location/Qualifiers

FT CDS 1..336

FT /*tag= a

FT /product= "Mechano-growth factor (MGF)"

FT /note= "This region comprises exons 3-6. The CDS does
 FT not include start codon"

FT /partial

XX

PN WO200136483-A1.

XX

PD 25-MAY-2001.

XX

PF 15-NOV-2000; 2000WO-GB04354.

XX

PR 15-NOV-1999; 99GB-0026968.

XX

PA (UNLO) UNIV COLLEGE LONDON.

XX

PI Goldspink G, Johnson I;

XX

DR WPI; 2001-355620/37.

DR P-PSDB; AAE02449.

XX

PT Use of mechano-growth factor, an isoform of Insulin-like Growth
 PT Factor-I, capable of reducing motoneurone loss, in the manufacture of a
 PT medicament for the treatment of neurological disorder -

XX

PS Claim 4; Page 53-54; 66pp; English.

XX

CC The present invention relates to use of mechano-growth factor (MGF),
 CC an Insulin-like Growth Factor-I (IGF-I) isoform in the manufacture of a
 CC medicament for the treatment of neurological disorder. The MGF is capable
 CC of reducing motoneurone loss by 20% or greater in response to nerve
 CC avulsion, and effects motoneurone rescue, preferably adult motoneurone
 CC rescue. The MGF polynucleotide and polypeptide are useful in the
 CC manufacture of a medicament for the treatment of a neurological disorder,
 CC including a disorder of motoneurons and/or neurodegenerative disorder,

CC e.g., amyotrophic lateral sclerosis, spinal muscular atrophy, progressive
 CC spinal muscular atrophy, infantile or juvenile muscular atrophy,
 CC poliomyelitis or post-polio syndrome, a disorder caused by exposure to a
 CC toxin, motoneurone trauma, a motoneurone lesion or nerve damage, an
 CC injury that affects motoneurons, motoneurone loss associated with aging,
 CC autosomal or sex-linked muscular dystrophy, diabetic neuropathy,
 CC peripheral neuropathies, Alzheimer's disease and Parkinson's disease.
 CC The present sequence is rabbit IGF-I isoform MGF cDNA. MGF is a muscle
 CC isoform having extracellular (Ec) domain, hence also referred as
 CC IGF-I-Ec. The MGF protein comprises amino acid sequences encoded by
 CC nucleic acid sequence of IGF-I exons 4, 5 and 6 in the reading frame
 CC of MGF.

XX

SQ Sequence 523 BP; 154 A; 129 C; 142 G; 98 T; 0 other;

Query Match 100.0%; Score 523; DB 22; Length 523;
 Best Local Similarity 100.0%; Pred. No. 5.1e-144;
 Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
      |||
Db      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

Qy     61 AGGGGCTTTTATTTCAACAAGCCCAAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
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Qy    121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
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Db    121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy    181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
      |||
Db    181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240

Qy    241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
      |||
Db    241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300

Qy    301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
      |||
Db    301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360

Qy    361 CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTG 420
      |||
Db    361 CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTG 420

Qy    421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480
      |||
Db    421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480

Qy    481 CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACATTTC 523
      |||
Db    481 CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACATTTC 523

```

RESULT 2

AAS16879

ID AAS16879 standard; cDNA; 523 BP.

XX

AC AAS16879;

XX

DT 25-FEB-2002 (first entry)

XX

DE Rabbit mechano-growth factor (MGF) cDNA.

XX

KW Rabbit; mechano-growth factor; insulin-like growth factor I; IGF-I; MGF;
KW neuroprotective; nerve damage; peripheral nervous system; nerve severing;
KW muscle; neurological disorder; motoneuron loss; motoneuron disorder; ss;
KW nerve avulsion.

XX

OS Oryctolagus cuniculus.

XX

FH Key Location/Qualifiers

FT CDS 1..336

FT /*tag= a

FT /product= "Rabbit MGF"

FT /partial

FT /note= "No start codon"

FT exon 1..76

FT /*tag= b

FT /number= 3

FT exon 77..259

FT /*tag= c

FT /number= 4

FT exon 260..309

FT /*tag= d

FT /number= 5

FT exon 311..333

FT /*tag= e

FT /number= 6

XX

PN WO200185781-A2.

XX

PD 15-NOV-2001.

XX

PF 10-MAY-2001; 2001WO-GB02054.

XX

PR 10-MAY-2000; 2000GB-0011278.

XX

PA (UNLO) UNIV COLLEGE LONDON.

PA (EGRI-) EAST GRINSTEAD MEDICAL RES TRUST.

XX

PI Goldspink G, Terenghi G;

XX

DR WPI; 2002-055585/07.

DR P-PSDB; AAU10561.

XX

PT Use of insulin-like growth factor I (IGF-I) isoform known as

PT mechano-growth factor which is encoded by IGF-I exons 4,5,6 and has

PT ability to reduce motoneuron loss in response to nerve avulsion, to

PT treat nerve damage -

XX

PS Disclosure; Fig 7; 65pp; English.

XX

CC The invention relates to the use of an insulin-like growth factor I
CC (IGF-I) isoform, known as mechano-growth factor (MGF), in the manufacture
CC of a medicament for treating nerve damage in the peripheral nervous
CC system, or for treating nerve damage by localising MGF at the site of
CC damage. The nerve damage may include severing of a nerve. The treatment
CC may be combined with another treatment (such as a polypeptide growth
CC factor other than MGF) that prevents or diminishes degeneration of the
CC target organ (for example, muscle) which the damaged nerve innervates,
CC whereby the treatment of the muscle with MGF or a polynucleotide encoding
CC MGF prevents or diminishes degeneration. The method is useful for
CC treating neurological disorders, preferably motoneuron disorders. These
CC methods can reduce motoneuron loss by 20% or greater in response to nerve
CC avulsion. This sequence represents cDNA encoding the rabbit MGF.

XX

SQ Sequence 523 BP; 154 A; 129 C; 142 G; 98 T; 0 other;

Query Match 100.0%; Score 523; DB 24; Length 523;
Best Local Similarity 100.0%; Pred. No. 5.1e-144;
Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
|||
Db 1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

Qy 61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGGCACCTCAG 120
|||
Db 61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGGCACCTCAG 120

Qy 121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
|||
Db 121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy 181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
|||
Db 181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240

Qy 241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
|||
Db 241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300

Qy 301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
|||
Db 301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360

Qy 361 CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTTG 420
|||
Db 361 CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTTG 420

Qy 421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480
|||
Db 421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480

Qy 481 CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACATTC 523
|||
Db 481 CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACATTC 523

RESULT 3

AAT84893

ID AAT84893 standard; cDNA; 553 BP.

XX

AC AAT84893;

XX

DT 14-APR-1998 (first entry)

XX

DE Rabbit insulin like growth factor 1 encoding cDNA.

XX

KW Insulin like growth factor 1; IGF-1; Ec peptide; muscle disorder;
KW heart; neuromuscular disease; primer; ss.

XX

OS Oryctolagus cuniculus.

XX

FH Key Location/Qualifiers

FT CDS 1..366

FT /*tag= a

FT /product= "IGF-1"

XX

PN WO9733997-A1.

XX

PD 18-SEP-1997.

XX

PF 11-MAR-1997; 97WO-GB00658.

XX

PR 11-MAR-1996; 96GB-0005124.

XX

PA (UNLO) ROYAL FREE HOSPITAL SCHOOL MED.

XX

PI Goldspink G;

XX

DR WPI; 1997-470877/43.

DR P-PSDB; AAW23301.

XX

PT Use of insulin like growth factor I characterised by presence of Ec
PT peptide - to treat humans or animals, particularly muscle disorders,
PT heart conditions or neuromuscular diseases

XX

PS Disclosure; Fig 3; 33pp; English.

XX

CC A use of insulin like growth factor I (IGF-1) has been developed, and
CC is characterised by the presence of the Ec peptide, or a functional
CC equivalent, in the treatment or therapy of a human or animal. The IGF-1
CC polypeptide can be used to treat muscular disorders, e.g. Duchenne or
CC Becker muscular dystrophy, autosomal dystrophies and related progressive
CC skeletal muscle weakness and wasting, muscle atrophy in ageing humans,
CC spinal cord injury induced muscle atrophy and neuromuscular diseases,
CC and cardiac disorders, e.g. diseases where promotion of cardiac muscle
CC protein synthesis is a beneficial treatment, cardiomyopathies and acute
CC heart failure or insult, specifically myocarditis or myocardial
CC infarction. It can also be used to promote bone fracture healing and
CC maintenance of bone in old age. The present sequence encodes rabbit
CC IGF-1 used in the present specification.

XX

SQ Sequence 553 BP; 159 A; 142 C; 147 G; 105 T; 0 other;

Query Match 100.0%; Score 523; DB 18; Length 553;
 Best Local Similarity 100.0%; Pred. No. 5.3e-144;
 Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db     91 AGGGGCTTTTATTTCAACAAGCCCAAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 150

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Qy    181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240
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Qy    241 ATGCCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
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Db    271 ATGCCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 330

Qy    301 AGAAGGAAAGGAAGTACATTTGAAGAACAACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
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Db    331 AGAAGGAAAGGAAGTACATTTGAAGAACAACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 390

Qy    361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
      |||
Db    391 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 450

Qy    421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480
      |||
Db    451 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 510

Qy    481 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
      |||
Db    511 CAAAGATGGCATTTCCCCCAATGAAATACACAAGTAAACATTC 553
  
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RESULT 4

AAD06398

ID AAD06398 standard; cDNA; 517 BP.

XX

AC AAD06398;

XX

DT 10-AUG-2001 (first entry)

XX

DE Human IGF-I isoform mechano-growth factor (MGF) cDNA.

XX

KW Human; IGF-I isoform; Insulin-like Growth Factor-I; MGF;

KW mechano-growth factor; neurological disorder; neurodegenerative disorder;

KW amyotrophic lateral sclerosis; spinal muscular atrophy; muscular atrophy;

KW poliomyelitis; post-polio syndrome; toxin; motoneurone disorder;

KW nerve damage; autosomal muscular dystrophy; diabetic neuropathy;

KW sex-linked muscular dystrophy; peripheral neuropathy;
 KW Alzheimer's disease; Parkinson's disease; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..333
 FT /*tag= a
 FT /product= "Mechano-growth factor (MGF)"
 FT /note= "This region comprises exons 3-6. The CDS does
 FT not include start codon"
 FT /partial
 XX
 PN WO200136483-A1.
 XX
 PD 25-MAY-2001.
 XX
 PF 15-NOV-2000; 2000WO-GB04354.
 XX
 PR 15-NOV-1999; 99GB-0026968.
 XX
 PA (UNLO) UNIV COLLEGE LONDON.
 XX
 PI Goldspink G, Johnson I;
 XX
 DR WPI; 2001-355620/37.
 DR P-PSDB; AAE02447.
 XX
 PT Use of mechano-growth factor, an isoform of Insulin-like Growth
 PT Factor-I, capable of reducing motoneurone loss, in the manufacture of a
 PT medicament for the treatment of neurological disorder -
 XX
 PS Claim 4; Page 49-50; 66pp; English.
 XX
 CC The present invention relates to use of mechano-growth factor (MGF),
 CC an Insulin-like Growth Factor-I (IGF-I) isoform in the manufacture of a
 CC medicament for the treatment of neurological disorder. The MGF is capable
 CC of reducing motoneurone loss by 20% or greater in response to nerve
 CC avulsion, and effects motoneurone rescue, preferably adult motoneurone
 CC rescue. The MGF polynucleotide and polypeptide are useful in the
 CC manufacture of a medicament for the treatment of a neurological disorder,
 CC including a disorder of motoneurons and/or neurodegenerative disorder,
 CC e.g., amyotrophic lateral sclerosis, spinal muscular atrophy, progressive
 CC spinal muscular atrophy, infantile or juvenile muscular atrophy,
 CC poliomyelitis or post-polio syndrome, a disorder caused by exposure to a
 CC toxin, motoneurone trauma, a motoneurone lesion or nerve damage, an
 CC injury that affects motoneurons, motoneurone loss associated with aging,
 CC autosomal or sex-linked muscular dystrophy, diabetic neuropathy,
 CC peripheral neuropathies, Alzheimer's disease and Parkinson's disease.
 CC The present sequence is human IGF-I isoform MGF cDNA. MGF is a muscle
 CC isoform having extracellular (Ec) domain, hence also referred as
 CC IGF-I-Ec. The MGF protein comprises amino acid sequences encoded by
 CC nucleic acid sequence of IGF-I exons 4, 5 and 6 in the reading frame
 CC of MGF.
 XX
 SQ Sequence 517 BP; 150 A; 130 C; 139 G; 98 T; 0 other;

Query Match 89.4%; Score 467.4; DB 22; Length 517;
 Best Local Similarity 96.2%; Pred. No. 1.3e-127;
 Matches 501; Conservative 0; Mismatches 16; Indels 4; Gaps 2;

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Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
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Db      1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

Qy     61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
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Db     61 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120

Qy    121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
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Db    121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180

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Db    181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC 240

Qy    241 ATGCCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
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Db    241 ATGCCCCAAGACCCAGAAGTATCAGCCCCATCTACCAACAAGAACACGAAGTCTCA---G 297

Qy    301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
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Db    298 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 357

Qy    361 CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
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Db    358 CAGGATGTA-GAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 416

Qy    421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480
      |||
Db    417 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 476

Qy    481 CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACAT 521
      |||
Db    477 CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACAT 517
  
```

RESULT 5

AAS16877

ID AAS16877 standard; cDNA; 517 BP.

XX

AC AAS16877;

XX

DT 25-FEB-2002 (first entry)

XX

DE Human mechano-growth factor (MGF) cDNA.

XX

KW Human; mechano-growth factor; insulin-like growth factor I; IGF-I; MGF;
 KW neuroprotective; nerve damage; peripheral nervous system; nerve severing;
 KW muscle; neurological disorder; motoneuron loss; motoneuron disorder; ss;
 KW nerve avulsion.

XX

OS Homo sapiens.

XX

Key	Location/Qualifiers
FT CDS	1..333
FT	/*tag= a
FT	/product= "Human MGF"
FT	/partial
FT	/note= "No start codon"
FT exon	1..76
FT	/*tag= b
FT	/number= 3
FT exon	77..259
FT	/*tag= c
FT	/number= 4
FT exon	260..307
FT	/*tag= d
FT	/number= 5
FT exon	308..330
FT	/*tag= e
FT	/number= 6

XX

PN WO200185781-A2.

XX

PD 15-NOV-2001.

XX

PF 10-MAY-2001; 2001WO-GB02054.

XX

PR 10-MAY-2000; 2000GB-0011278.

XX

PA (UNLO) UNIV COLLEGE LONDON.

PA (EGRI-) EAST GRINSTEAD MEDICAL RES TRUST.

XX

PI Goldspink G, Terenghi G;

XX

DR WPI; 2002-055585/07.

DR P-PSDB; AAU10559.

XX

PT Use of insulin-like growth factor I (IGF-I) isoform known as

PT mechano-growth factor which is encoded by IGF-I exons 4,5,6 and has

PT ability to reduce motoneuron loss in response to nerve avulsion, to

PT treat nerve damage -

XX

PS Claim 11; Fig 5; 65pp; English.

XX

CC The invention relates to the use of an insulin-like growth factor I

CC (IGF-I) isoform, known as mechano-growth factor (MGF), in the manufacture

CC of a medicament for treating nerve damage in the peripheral nervous

CC system, or for treating nerve damage by localising MGF at the site of

CC damage. The nerve damage may include severing of a nerve. The treatment

CC may be combined with another treatment (such as a polypeptide growth

CC factor other than MGF) that prevents or diminishes degeneration of the

CC target organ (for example, muscle) which the damaged nerve innervates,

CC whereby the treatment of the muscle with MGF or a polynucleotide encoding

CC MGF prevents or diminishes degeneration. The method is useful for

CC treating neurological disorders, preferably motorneuron disorders. These

CC methods can reduce motoneuron loss by 20% or greater in response to nerve

CC avulsion. This sequence represents cDNA encoding the human MGF.

XX

SQ Sequence 517 BP; 150 A; 130 C; 139 G; 98 T; 0 other;

Query Match 89.4%; Score 467.4; DB 24; Length 517;
Best Local Similarity 96.2%; Pred. No. 1.3e-127;
Matches 501; Conservative 0; Mismatches 16; Indels 4; Gaps 2;

```
Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
      |||
Db      1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

Qy     61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
      |||
Db     61 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120

Qy    121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
      |||
Db    121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180

Qy    181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240
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Db    181 TGTGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC 240

Qy    241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
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Db    241 ATGCCCAAGACCCAGAAGTATCAGCCCCATCTACCAACAAGAACACGAAGTCTCA---G 297

Qy    301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
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Db    298 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 357

Qy    361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
      |||
Db    358 CAGGATGTA-GAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 416

Qy    421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480
      |||
Db    417 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 476

Qy    481 CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACAT 521
      |||
Db    477 CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACAT 517
```

RESULT 6

AAD06405

ID AAD06405 standard; cDNA; 471 BP.

XX

AC AAD06405;

XX

DT 10-AUG-2001 (first entry)

XX

DE Rabbit liver-type IGF-I isoform (L.IGF-I) cDNA.

XX

KW Rabbit; IGF-I isoform; Insulin-like Growth Factor-I; MGF;

KW mechano-growth factor; neurological disorder; neurodegenerative disorder;

KW amyotrophic lateral sclerosis; spinal muscular atrophy; muscular atrophy;

KW poliomyelitis; post-polio syndrome; toxin; motoneurone disorder;

KW nerve damage; autosomal muscular dystrophy; diabetic neuropathy;
 KW sex-linked muscular dystrophy; peripheral neuropathy;
 KW Alzheimer's disease; Parkinson's disease; liver; L.IGF-I; ss.
 XX
 OS *Oryctolagus cuniculus*.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..318
 FT /*tag= a
 FT /product= "Liver-type IGF-I isoform (L.IGF-I)"
 FT /transl_except= (pos:7..9, aa:Gln)
 FT /transl_except= (pos:25..27, aa:Gln)
 FT /note= "These translation exceptions occur while decoding
 FT the alternative version of the protein (AAE02456).
 FT The CDS comprises exons 3, 4 and 6 and
 FT does not include start codon"
 FT /partial
 XX
 PN WO200136483-A1.
 XX
 PD 25-MAY-2001.
 XX
 PF 15-NOV-2000; 2000WO-GB04354.
 XX
 PR 15-NOV-1999; 99GB-0026968.
 XX
 PA (UNLO) UNIV COLLEGE LONDON.
 XX
 PI Goldspink G, Johnson I;
 XX
 DR WPI; 2001-355620/37.
 DR P-PSDB; AAE02452, AAE02456.
 XX
 PT Use of mechano-growth factor, an isoform of Insulin-like Growth
 PT Factor-I, capable of reducing motoneurone loss, in the manufacture of a
 PT medicament for the treatment of neurological disorder -
 XX
 PS Disclosure; Page 59-60; 66pp; English.
 XX
 CC The present invention relates to use of mechano-growth factor (MGF),
 CC an Insulin-like Growth Factor-I (IGF-I) isoform in the manufacture of a
 CC medicament for the treatment of neurological disorder. The MGF is capable
 CC of reducing motoneurone loss by 20% or greater in response to nerve
 CC avulsion, and effects motoneurone rescue, preferably adult motoneurone
 CC rescue. The MGF polynucleotide and polypeptide are useful in the
 CC manufacture of a medicament for the treatment of a neurological disorder,
 CC including a disorder of motoneurons and/or neurodegenerative disorder,
 CC e.g., amyotrophic lateral sclerosis, spinal muscular atrophy, progressive
 CC spinal muscular atrophy, infantile or juvenile muscular atrophy,
 CC poliomyelitis or post-polio syndrome, a disorder caused by exposure to a
 CC toxin, motoneurone trauma, a motoneurone lesion or nerve damage, an
 CC injury that affects motoneurons, motoneurone loss associated with aging,
 CC autosomal or sex-linked muscular dystrophy, diabetic neuropathy,
 CC peripheral neuropathies, Alzheimer's disease and Parkinson's disease.
 CC The present sequence is rabbit liver-type IGF-I isoform (L.IGF-I) cDNA.
 CC The L.IGF-I protein comprises amino acid sequences encoded by
 CC nucleic acid sequence of IGF-I exons 4 and 6.

XX

SQ Sequence 471 BP; 132 A; 118 C; 131 G; 90 T; 0 other;

Query Match 78.2%; Score 409; DB 22; Length 471;
Best Local Similarity 90.1%; Pred. No. 2e-110;
Matches 471; Conservative 0; Mismatches 0; Indels 52; Gaps 1;

```
Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
      |||
Db      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

Qy     61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
      |||
Db     61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120

Qy    121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
      |||
Db    121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy    181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240
      |||
Db    181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240

Qy    241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
      |||
Db    241 ATGCCCAAGACTCAG----- 255

Qy    301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
      |||
Db    256 -----AAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 308

Qy    361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
      |||
Db    309 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 368

Qy    421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480
      |||
Db    369 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 428

Qy    481 CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACATTTC 523
      |||
Db    429 CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACATTTC 471
```

RESULT 7

AAS16884

ID AAS16884 standard; cDNA; 471 BP.

XX

AC AAS16884;

XX

DT 25-FEB-2002 (first entry)

XX

DE Rabbit insulin-like growth factor I liver-type isoform (L.IGF-I) cDNA.

XX

KW Rabbit; mechano-growth factor; insulin-like growth factor I; IGF-I; MGF;
KW neuroprotective; nerve damage; peripheral nervous system; nerve severing;
KW muscle; neurological disorder; motoneuron loss; motoneuron disorder; ss;

KW nerve avulsion; insulin-like growth factor I liver-type isoform; L.IGF-I;
XX
OS Oryctolagus cuniculus.

XX
FH Key Location/Qualifiers
FT CDS 1..318
FT /*tag= a
FT /product= "Rabbit L.IGF-I"
FT /partial
FT /note= "No start codon"
FT exon 1..75
FT /*tag= b
FT /number= exon 3
FT exon 76..258
FT /*tag= c
FT /number= exon 4
FT exon 259..315
FT /*tag= d
FT /number= exon 6

XX
PN WO200185781-A2.
XX
PD 15-NOV-2001.
XX
PF 10-MAY-2001; 2001WO-GB02054.
XX
PR 10-MAY-2000; 2000GB-0011278.
XX
PA (UNLO) UNIV COLLEGE LONDON.
PA (EGRI-) EAST GRINSTEAD MEDICAL RES TRUST.

XX
PI Goldspink G, Terenghi G;

XX
DR WPI; 2002-055585/07.
DR P-PSDB; AAU10564.

XX
PT Use of insulin-like growth factor I (IGF-I) isoform known as
PT mechano-growth factor which is encoded by IGF-I exons 4,5,6 and has
PT ability to reduce motoneuron loss in response to nerve avulsion, to
PT treat nerve damage -

XX
PS Disclosure; Fig 10; 65pp; English.

XX
CC The invention relates to the use of an insulin-like growth factor I
CC (IGF-I) isoform, known as mechano-growth factor (MGF), in the manufacture
CC of a medicament for treating nerve damage in the peripheral nervous
CC system, or for treating nerve damage by localising MGF at the site of
CC damage. The nerve damage may include severing of a nerve. The treatment
CC may be combined with another treatment (such as a polypeptide growth
CC factor other than MGF) that prevents or diminishes degeneration of the
CC target organ (for example, muscle) which the damaged nerve innervates,
CC whereby the treatment of the muscle with MGF or a polynucleotide encoding
CC MGF prevents or diminishes degeneration. The method is useful for
CC treating neurological disorders, preferably motoneuron disorders. These
CC methods can reduce motoneuron loss by 20% or greater in response to nerve
CC avulsion. This sequence represents cDNA encoding the rabbit insulin-like
CC growth factor I liver-type isoform (L.IGF-I) used in experiments on

CC motoneuron loss.

XX

SQ Sequence 471 BP; 132 A; 118 C; 131 G; 90 T; 0 other;

Query Match 78.2%; Score 409; DB 24; Length 471;
Best Local Similarity 90.1%; Pred. No. 2e-110;
Matches 471; Conservative 0; Mismatches 0; Indels 52; Gaps 1;

```
Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
      |||
Db      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

Qy     61 AGGGGCTTTTATTTCAACAAGCCCAAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
      |||
Db     61 AGGGGCTTTTATTTCAACAAGCCCAAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120

Qy    121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
      |||
Db    121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy    181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240
      |||
Db    181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240

Qy    241 ATGCCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
      |||
Db    241 ATGCCCCAAGACTCAG----- 255

Qy    301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
      |||
Db    256 -----AAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 308

Qy    361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
      |||
Db    309 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 368

Qy    421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGTATCACATTT 480
      |||
Db    369 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGTATCACATTT 428

Qy    481 CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACATTTC 523
      |||
Db    429 CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACATTTC 471
```

RESULT 8

AAD06399

ID AAD06399 standard; cDNA; 539 BP.

XX

AC AAD06399;

XX

DT 10-AUG-2001 (first entry)

XX

DE Rat IGF-I isoform mechano-growth factor (MGF) cDNA.

XX

KW Rat; IGF-I isoform; Insulin-like Growth Factor-I; MGF;

KW mechano-growth factor; neurological disorder; neurodegenerative disorder;

KW amyotrophic lateral sclerosis; spinal muscular atrophy; muscular atrophy;
KW poliomyelitis; post-polio syndrome; toxin; motoneurone disorder;
KW nerve damage; autosomal muscular dystrophy; diabetic neuropathy;
KW sex-linked muscular dystrophy; peripheral neuropathy;
KW Alzheimer's disease; Parkinson's disease; ss.

XX

OS Rattus sp.

XX

FH Key Location/Qualifiers

FT CDS 1..336

FT /*tag= a

FT /product= "Mechano-growth factor (MGF)"

FT /note= "This region comprises exons 3-6. The CDS does

FT not include start codon"

FT /partial

XX

PN WO200136483-A1.

XX

PD 25-MAY-2001.

XX

PF 15-NOV-2000; 2000WO-GB04354.

XX

PR 15-NOV-1999; 99GB-0026968.

XX

PA (UNLO) UNIV COLLEGE LONDON.

XX

PI Goldspink G, Johnson I;

XX

DR WPI; 2001-355620/37.

DR P-PSDB; AAE02448.

XX

PT Use of mechano-growth factor, an isoform of Insulin-like Growth
PT Factor-I, capable of reducing motoneurone loss, in the manufacture of a
PT medicament for the treatment of neurological disorder -

XX

PS Claim 4; Page 51-52; 66pp; English.

XX

CC The present invention relates to use of mechano-growth factor (MGF),
CC an Insulin-like Growth Factor-I (IGF-I) isoform in the manufacture of a
CC medicament for the treatment of neurological disorder. The MGF is capable
CC of reducing motoneurone loss by 20% or greater in response to nerve
CC avulsion, and effects motoneurone rescue, preferably adult motoneurone
CC rescue. The MGF polynucleotide and polypeptide are useful in the
CC manufacture of a medicament for the treatment of a neurological disorder,
CC including a disorder of motoneurons and/or neurodegenerative disorder,
CC e.g., amyotrophic lateral sclerosis, spinal muscular atrophy, progressive
CC spinal muscular atrophy, infantile or juvenile muscular atrophy,
CC poliomyelitis or post-polio syndrome, a disorder caused by exposure to a
CC toxin, motoneurone trauma, a motoneurone lesion or nerve damage, an
CC injury that affects motoneurons, motoneurone loss associated with aging,
CC autosomal or sex-linked muscular dystrophy, diabetic neuropathy,
CC peripheral neuropathies, Alzheimer's disease and Parkinson's disease.
CC The present sequence is rat IGF-I isoform MGF cDNA. MGF is a muscle
CC isoform having extracellular (Ec) domain, hence also referred as
CC IGF-I-Ec. The MGF protein comprises amino acid sequences encoded by
CC nucleic acid sequence of IGF-I exons 4, 5 and 6 in the reading frame
CC of MGF.

XX

SQ Sequence 539 BP; 161 A; 136 C; 139 G; 103 T; 0 other;

Query Match 68.2%; Score 356.8; DB 22; Length 539;
Best Local Similarity 82.3%; Pred. No. 5.1e-95;
Matches 436; Conservative 0; Mismatches 87; Indels 7; Gaps 2;

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Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
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Db      1 GGACCAGAGACCCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60

Qy     61 AGGGGCTTTTATTTCAACAAGCCCAAGGATACGGCTCCAGCAGTCGGAGGGGCACCTCAG 120
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     61 AGGGGCTTTTACTTCAACAAGCCCAAGTCTATGGCTCCAGCATTCCGAGGGGCACCACAG 120

Qy    121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
        || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    121 ACGGGCATTGTGGATGAGTGTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy    181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240
        ||||| || || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCAGCGCCACACTGAC 240

Qy    241 ATGCCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    241 ATGCCCCAAGACTCAGAAGTCCCAGCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300

Qy    301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360

Qy    361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
        ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTCACCGCAAGATCCTTTG 420

Qy    421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA-----AAAAATAAGTTTGTATC 474
        || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    421 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 480

Qy    475 ACATTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTTC 523
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    481 TCATTTCAAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTTC 530
```

RESULT 9

AAS16878

ID AAS16878 standard; cDNA; 539 BP.

XX

AC AAS16878;

XX

DT 25-FEB-2002 (first entry)

XX

DE Rat mechano-growth factor (MGF) cDNA.

XX

KW Rat; mechano-growth factor; insulin-like growth factor I; IGF-I; MGF;
KW neuroprotective; nerve damage; peripheral nervous system; nerve severing;
KW muscle; neurological disorder; motoneuron loss; motoneuron disorder; ss;

KW nerve avulsion.

XX

OS Rattus sp.

XX

FH Key Location/Qualifiers

FT CDS 1..336

FT /*tag= a

FT /product= "Rat MGF"

FT /partial

FT /note= "No start codon"

FT exon 1..75

FT /*tag= b

FT /number= exon 3

FT exon 76..258

FT /*tag= c

FT /number= exon 4

FT exon 259..309

FT /*tag= d

FT /number= exon 5

FT exon 310..333

FT /*tag= e

FT /number= exon 6

XX

PN WO200185781-A2.

XX

PD 15-NOV-2001.

XX

PF 10-MAY-2001; 2001WO-GB02054.

XX

PR 10-MAY-2000; 2000GB-0011278.

XX

PA (UNLO) UNIV COLLEGE LONDON.

PA (EGRI-) EAST GRINSTEAD MEDICAL RES TRUST.

XX

PI Goldspink G, Terenghi G;

XX

DR WPI; 2002-055585/07.

DR P-PSDB; AAU10560.

XX

PT Use of insulin-like growth factor I (IGF-I) isoform known as

PT mechano-growth factor which is encoded by IGF-I exons 4,5,6 and has

PT ability to reduce motoneuron loss in response to nerve avulsion, to

PT treat nerve damage -

XX

PS Disclosure; Fig 6; 65pp; English.

XX

CC The invention relates to the use of an insulin-like growth factor I

CC (IGF-I) isoform, known as mechano-growth factor (MGF), in the manufacture

CC of a medicament for treating nerve damage in the peripheral nervous

CC system, or for treating nerve damage by localising MGF at the site of

CC damage. The nerve damage may include severing of a nerve. The treatment

CC may be combined with another treatment (such as a polypeptide growth

CC factor other than MGF) that prevents or diminishes degeneration of the

CC target organ (for example, muscle) which the damaged nerve innervates,

CC whereby the treatment of the muscle with MGF or a polynucleotide encoding

CC MGF prevents or diminishes degeneration. The method is useful for

CC treating neurological disorders, preferably motorneuron disorders. These

CC methods can reduce motoneuron loss by 20% or greater in response to nerve
CC avulsion. This sequence represents cDNA encoding the rat MGF.
XX
SQ Sequence 539 BP; 161 A; 136 C; 139 G; 103 T; 0 other;

Query Match 68.2%; Score 356.8; DB 24; Length 539;
Best Local Similarity 82.3%; Pred. No. 5.1e-95;
Matches 436; Conservative 0; Mismatches 87; Indels 7; Gaps 2;

```
Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
        ||||| ||||| || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1 GGACCAGAGACCCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60

Qy     61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     61 AGGGGCTTTTACTTCAACAAGCCACAGTCTATGGCTCCAGCATTCCGGAGGGCACCACAG 120

Qy    121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
        || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    121 ACGGCATTGTGGATGAGTGTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy    181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240
        |||| | | ||||| ||||| |||| | | |||| | | ||||| ||||| |||||
Db    181 TGTGTCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCAGCGCCACACTGAC 240

Qy    241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
        ||||| ||||| ||||| |||| | |||| | ||||| |||| | |||||
Db    241 ATGCCCAAGACTCAGAAGTCCCAGCCCCTATCGACACACAAGAAAAGGAAGCTGCAAAGG 300

Qy    301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360

Qy    361 CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTTG 420
        || ||||| |||| | |||| | |||| | |||| | |||| | |||| | |||||
Db    361 CAGAATGTAGGAGGAGCCTCCCGAGGAACAGAAAATGCCACGTACCGCAAGATCCTTTG 420

Qy    421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA-----AAAAATAAGTTTGATC 474
        || | ||||| |||| | |||| | |||| | |||| | |||| | |||| | |||||
Db    421 CTGCTTGAGCAACCTGCAAAACATCGGAACACCTGCCAAATATCAATAATGAGTTCAATA 480

Qy    475 ACATTTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTTC 523
        ||||| |||| | ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    481 TCATTTTCAGAGATGGGCATTTCCCTCAATGAAATACACAAGTAAACATTTC 530
```

RESULT 10

ABV76185

ID ABV76185 standard; cDNA; 651 BP.

XX

AC ABV76185;

XX

DT 07-MAR-2003 (first entry)

XX

DE Mouse insulin-like growth factor IB cDNA.

XX

KW Insulin-like growth factor IB; IGF-IB; mouse; mRNA; assay;

KW nucleic acid detection; gene; ss.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT CDS 73..474
 FT /*tag= a
 FT /product= "IGF-IB"
 XX
 PN WO200297390-A2.
 XX
 PD 05-DEC-2002.
 XX
 PF 31-MAY-2002; 2002WO-SE01056.
 XX
 PR 01-JUN-2001; 2001SE-0001934.
 XX
 PA (BIOV-) BIOVITRUM AB.
 XX
 PI Parrow V, Rosengren L;
 XX
 DR WPI; 2003-129529/12.
 XX
 PT Quantitating a target nucleic acid in a sample comprises immobilizing,
 PT on a solid support, a sample comprising a target nucleic acid, and
 PT detecting and quantitating signals generated from the antisense and
 PT sense probes -
 XX
 PS Example 1; Page 16-17; 18pp; English.
 XX
 CC The present sequence is that of cDNA encoding murine insulin-like
 CC growth factor 1B (IGF-IB). The cDNA was used in an example of the
 CC method of the invention to generate probes for determination of
 CC IGF-IB RNA. The method comprises a quantitative hybridisation
 CC assay for analysis of mRNA in a target nucleic acid (TNA) sample.
 CC It involves: (i) immobilising the TNA sample on a solid support;
 CC (ii) contacting a labelled antisense probe to a first portion of the
 CC TNA, and a labelled sense probe to a second portion of the TNA;
 CC (iii) detecting and quantitating the signals generated from the
 CC hybridised probes; and (iv) determining the value represented by
 CC the antisense probe signal minus the sense probe signal, the value
 CC being proportional to the amount of mRNA in the TNA sample. In an
 CC example of the method, a cDNA clone containing 60 nucleotides from
 CC exon 2 and 179 nucleotides from exon 3 of the mouse IGF-IB gene was
 CC cloned into pGEN-4Z vector. Linearisation of the plasmid with
 CC EcoRI allowed transcription of a 250-nucleotide antisense probe
 CC using T7 polymerase. Linearisation with HindIII allowed
 CC transcription of a sense probe of similar length using SP6
 CC polymerase (see ABV76186). The probes were purified and used to
 CC determine IGF-I RNA in mouse hepatocytes and also in rat hepatocytes.
 XX
 SQ Sequence 651 BP; 193 A; 185 C; 149 G; 124 T; 0 other;

Query Match 66.8%; Score 349.4; DB 25; Length 651;
 Best Local Similarity 82.8%; Pred. No. 8.3e-93;
 Matches 425; Conservative 0; Mismatches 81; Indels 7; Gaps 2;


```

XX
PR 20-NOV-1986; 86US-0929671.
PR 07-JAN-1986; 86US-0816662.
XX
PA (UNIW ) UNIV WASHINGTON.
XX
PI Krivi GG, Rotwein PS;
XX
DR WPI; 1987-200203/29.
XX
PT New pre-pro-insulin-like growth factor-1 protein - obtd. by
PT recombinant DNA procedures for use as growth promoters for
PT enhancing lactation, for stimulating cell proliferation etc.
XX
PS Example; Fig 5; 59pp; English.
XX
CC A 42 base oligonucleotide corresponding to the DNA sequence encoding
CC amino acids 10 to 23 of mature human IGF-I was synthesized (AAN70437).
CC The radiolabeled 42 mer was then employed to screen for IGF-I
CC containing DNA sequences in a human liver cDNA library. Insulin-
CC like growth factors-1A and -1B cDNAs were isolated from a human cDNA
CC library by using lambdagt 11 (AAN70435, AAN70436). The human IGF-1
CC genomic gene was isolated and mapped. It encodes at least two
CC preproinsulin-like growth factor-1 proteins. An essentially pure
CC preproinsulin-like growth factor-1 protein comprising the sequence
CC of amino acids shown in Figure six is claimed (AAP70277).
CC (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 818 BP; 232 A; 186 C; 187 G; 213 T; 0 other;

Query Match 63.9%; Score 334.4; DB 8; Length 818;
Best Local Similarity 84.6%; Pred. No. 2.4e-88;
Matches 445; Conservative 0; Mismatches 26; Indels 55; Gaps 4;

Qy 1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
   |||
Db 203 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 262

Qy 61 AGGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGGCACCTCAG 120
   |||
Db 263 AGGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGGCGCCTCAG 322

Qy 121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
   |||
Db 323 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 382

Qy 181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240
   |||
Db 383 TGCACACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC 442

Qy 241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
   |||
Db 443 ATGCCCAAGACCCAG----- 457

Qy 301 AGAAGGAAAGGAAGTACATTTGAAGAACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
   |||
Db 458 -----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 510

```


CC The methods are also useful as a screening tool for agents that modulate
CC the onset or progression of breast cancer. The breast cancer genes may be
CC used as diagnostic markers for the prediction or identification of the
CC malignant state of breast tissue, for confirming the type and progression
CC of cancer, and for drug screening and assays. The present sequence is a
CC coding sequence of the invention.

CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub.published_pct_sequences.

XX

SQ Sequence 7260 BP; 2330 A; 1415 C; 1240 G; 2275 T; 0 other;

Query Match 63.9%; Score 334.4; DB 24; Length 7260;
Best Local Similarity 84.6%; Pred. No. 5.7e-88;
Matches 445; Conservative 0; Mismatches 26; Indels 55; Gaps 4;

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Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
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Db      311 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 370

Qy      61 AGGGGCTTTTATTTCAACAAGCCCAAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
      |||
Db      371 AGGGGCTTTTATTTCAACAAGCCCAAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 430

Qy     121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
      |||
Db     431 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 490

Qy     181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240
      |||
Db     491 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC 550

Qy     241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
      |||
Db     551 ATGCCCAAGACCCAG----- 565

Qy     301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
      |||
Db     566 -----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 618

Qy     361 CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTTG 420
      |||
Db     619 CAGGATGTAGGAAGACCCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG 678

Qy     421 CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACAT 478
      |||
Db     679 CTCTGCACGAGTTACCTGTTAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACAT 738

Qy     479 TTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATT 523
      |||
Db     739 TTAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATT 784
```

RESULT 13

ABK84583

ID ABK84583 standard; cDNA; 7260 BP.

XX

AC ABK84583;
 XX
 DT 14-AUG-2002 (first entry)
 XX
 DE Human cDNA differentially expressed in granulocytic cells #1154.
 XX
 KW Human; ss; granulocytic cell; DNA chip; bacterial infection;
 KW viral infection; parasitic infection; protozoal infection;
 KW fungal infection; sterile inflammatory disease; psoriasis;
 KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
 KW cardiac reperfusion injury; renal reperfusion injury; ARDS;
 KW adult respiratory distress syndrome; inflammatory bowel disease;
 KW Crohn's disease; ulcerative colitis; periodontal disease;
 KW granulocyte activation; chronic inflammation; allergy.
 XX
 OS Homo sapiens.
 XX
 PN WO200228999-A2.
 XX
 PD 11-APR-2002.
 XX
 PF 03-OCT-2001; 2001WO-US30821.
 XX
 PR 03-OCT-2000; 2000US-237189P.
 XX
 PA (GENE-) GENE LOGIC INC.
 XX
 PI Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;
 XX
 DR WPI; 2002-435328/46.
 XX
 PT Detecting granulocyte activation by detecting differential expression
 PT of genes associated with granulocyte activation, which serves as
 PT diagnostic markers that is useful for monitoring disease states and
 PT drug toxicity -
 XX
 PS Claim 1; SEQ ID No 1154; 114pp; English.
 XX
 CC The invention relates to detecting (M1) granulocyte (GC) activation
 CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by
 CC DNA chip analysis as given in the specification, and comparing
 CC the expression level to an expression level in an unactivated
 CC GC, where differential expression of Gs is indicative of GCA.
 CC Also included are modulating (M2) GA by contacting GC with an agent
 CC that alters the expression of at least one gene in Gs; (2) screening (M3)
 CC for an agent capable of modulating GCA or an inflammation (especially
 CC chronic) in a tissue, an allergic response in a subject, exposure of a
 CC subject to a pathogen or sterile inflammatory disease using the
 CC gene expression profile; (3) detecting (M4) an inflammation (especially
 CC chronic) in a tissue, an allergic response in a subject, exposure of a
 CC subject to a pathogen or sterile inflammatory disease, by detecting the
 CC level of expression in a sample of the tissue of gene(s) from Gs, where
 CC the level of expression of the gene is indicative of inflammation;
 CC (4) treating (M5) an inflammation (especially chronic) or in a tissue,
 CC an allergic response in a subject, exposure of a subject to a pathogen
 CC or sterile inflammatory disease, by contacting a tissue having
 CC inflammation with an agent that modulates the expression of gene(s)

CC from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for
 CC modulating GA; M3 is useful for screening an agent capable of modulating
 CC GCA preferably in an inflammation in a tissue; M4 is useful for
 CC detecting an inflammation (especially chronic) in a tissue, an allergic
 CC response in a subject, exposure of a subject to a pathogen or sterile
 CC inflammatory disease (e.g. psoriasis, rheumatoid arthritis,
 CC glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal
 CC reperfusion injury, ARDS, adult respiratory distress syndrome,
 CC inflammatory bowel disease, Crohn's disease, ulcerative colitis,
 CC periodontal disease; also bacterial infection, viral infection,
 CC parasitic infection, protozoal infection, fungal infection and M5 is
 CC useful for treating one of the above conditions. The present
 CC sequence represents a gene differentially expressed in granulocytes.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX

SQ Sequence 7260 BP; 2330 A; 1415 C; 1240 G; 2275 T; 0 other;

Query Match 63.9%; Score 334.4; DB 24; Length 7260;
 Best Local Similarity 84.6%; Pred. No. 5.7e-88;
 Matches 445; Conservative 0; Mismatches 26; Indels 55; Gaps 4;

Qy	1	GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC	60
Db	311	GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC	370
Qy	61	AGGGGCTTTTATTTCAACAAGCCCAAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG	120
Db	371	AGGGGCTTTTATTTCAACAAGCCCAAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG	430
Qy	121	ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC	180
Db	431	ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT	490
Qy	181	TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC	240
Db	491	TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC	550
Qy	241	ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG	300
Db	551	ATGCCCAAGACCCAG-----	565
Qy	301	AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA	360
Db	566	-----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA	618
Qy	361	CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTTG	420
Db	619	CAGGATGTAGGAAGACCCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG	678
Qy	421	CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGTACACAT	478
Db	679	CTCTGCACGAGTTACCTGTTAAACTTTGGAACACCTACCAAAAAATAAGTTTGTATAACAT	738
Qy	479	TTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC	523

Db

739 TTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTTC 784

RESULT 14

ABN97244

ID ABN97244 standard; DNA; 7260 BP.

XX

AC ABN97244;

XX

DT 13-AUG-2002 (first entry)

XX

DE Gene #3742 used to diagnose liver cancer.

XX

KW Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic;
KW metastatic liver tumour; cytostatic; expression profile; disease state;
KW disease progression; drug toxicity; drug efficacy; drug metabolism.

XX

OS Homo sapiens.

XX

PN WO200229103-A2.

XX

PD 11-APR-2002.

XX

PF 02-OCT-2001; 2001WO-US30589.

XX

PR 02-OCT-2000; 2000US-237054P.

XX

PA (GENE-) GENE LOGIC INC.

XX

PI Horne D, Alvares C, Peres-Da-Silva S, Vockley JG;

XX

DR WPI; 2002-426119/45.

XX

PT Diagnosing and detecting the progression of liver cancer,
PT hepatocellular carcinoma or metastatic liver tumor in a patient,
PT involves detecting the level of expression of two or more genes in a
PT liver tissue sample -

XX

PS Claim 1; SEQ ID NO 3742; 298pp; English.

XX

CC The invention relates to a novel method for diagnosing and detecting the
CC progression of liver cancer, hepatocellular carcinoma or metastatic liver
CC tumour in a patient, and differentiating metastatic liver cancer from
CC hepatocellular carcinoma in a patient, involving detecting the level of
CC expression of two or more genes represented in ABN93503-ABN97455 in a
CC tissue sample. The method of the invention has hepatotropic, and
CC cytostatic activity. The method is useful for diagnosing and detecting
CC the progression of liver cancer, hepatocellular carcinoma and metastatic
CC liver carcinoma in a patient. The method is useful for identifying
CC expression profiles which serve as useful diagnostic markers as well as
CC markers that can be used to monitor disease states, disease progression,
CC drug toxicity, drug efficacy and drug metabolism.

CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX

SQ Sequence 7260 BP; 2330 A; 1415 C; 1240 G; 2275 T; 0 other;

Query Match 63.9%; Score 334.4; DB 24; Length 7260;
Best Local Similarity 84.6%; Pred. No. 5.7e-88;
Matches 445; Conservative 0; Mismatches 26; Indels 55; Gaps 4;

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Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
      |||
Db      311 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 370

Qy      61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
      |||
Db      371 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 430

Qy     121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
      |||
Db     431 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 490

Qy     181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240
      |||
Db     491 TGTGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC 550

Qy     241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
      |||
Db     551 ATGCCCAAGACCCAG----- 565

Qy     301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
      |||
Db     566 -----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 618

Qy     361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
      |||
Db     619 CAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG 678

Qy     421 CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACAT 478
      |||
Db     679 CTCTGCACGAGTTACCTGTTAAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACAT 738

Qy     479 TTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTTC 523
      |||
Db     739 TTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTTC 784
```

RESULT 15

ABK64812

ID ABK64812 standard; DNA; 7260 BP.

XX

AC ABK64812;

XX

DT 18-JUN-2002 (first entry)

XX

DE Human benign prostatic hyperplasia gene #707.

XX

KW Human; benign prostatic hyperplasia; BPH; prostate cancer; gene; ds.

XX

OS Homo sapiens.

XX

PN WO200212440-A2.
 XX
 PD 14-FEB-2002.
 XX
 PF 07-AUG-2001; 2001WO-US24708.
 XX
 PR 07-AUG-2000; 2000US-223323P.
 PR 05-JUN-2001; 2001US-0873319.
 XX
 PA (GENE-) GENE LOGIC INC.
 PA (NISB) JAPAN TOBACCO INC.
 XX
 PI Munger WE, Kulkarni P, Getzenberg RH, Waga I, Yamamoto J;
 XX
 DR WPI; 2002-257476/30.
 XX
 PT Identifying drugs for and diagnosing benign prostatic hyperplasia, by
 PT detecting expression levels of one or more genes in prostate cells from
 PT patient that are differentially regulated compared to normal prostate
 PT cells -
 XX
 PS Disclosure; Page 391-393; 444pp; English.
 XX
 CC The invention relates to a method of diagnosing (I) the onset or
 CC progression of benign prostatic hyperplasia (BPH), or screening (II) for
 CC or identifying an agent that modulates the onset or progression of BPH.
 CC The method is based on changes in gene expression in BPH tissue isolated
 CC from patients exhibiting different clinical states of prostate
 CC hyperplasia as compared to normal prostate tissue. (I) comprises
 CC detecting the expression levels of one or more genes in prostate cells
 CC from the subject that are differentially regulated compared to normal
 CC prostate cells. (II) comprises preparing a first gene expression profile
 CC of BPH cells or BPH-like cell population, exposing the cells to the
 CC agent, preparing a second gene expression profile of the agent exposed
 CC cells, and comparing the first and second gene expression profiles.
 CC (I) is useful for diagnosing the onset or progression of BPH. (II) is
 CC useful for identifying an agent that modulates the onset or progression
 CC of BPH. The methods are useful to present information identifying
 CC the expression level in a tissue or cells, by comparing the expression
 CC level of genes given in the specification in the tissue or cells to the
 CC level of expression of gene in the database, and displaying the
 CC expression levels of at least one gene in the tissue or cell sample
 CC compared to the expression level in BPH. Agents using (II) are useful for
 CC treating BPH or prostate cancer. ABK64106-ABK64860 represent human
 CC benign prostatic hyperplasia gene sequences of the invention.
 XX
 SQ Sequence 7260 BP; 2330 A; 1415 C; 1240 G; 2275 T; 0 other;

Query Match 63.9%; Score 334.4; DB 24; Length 7260;
 Best Local Similarity 84.6%; Pred. No. 5.7e-88;
 Matches 445; Conservative 0; Mismatches 26; Indels 55; Gaps 4;

Qy 1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTTCGTGTGTGGAGAC 60
 |||||||||||||||||||
 Db 311 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTTCGTGTGTGGAGAC 370
 Qy 61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGGCACCTCAG 120

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      |||
Db      371 AGGGGCTTTTATTTCAACAAGCCCAAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 430
      |||
Qy      121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
      |||
Db      431 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 490
      |||
Qy      181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240
      |||
Db      491 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC 550
      |||
Qy      241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
      |||
Db      551 ATGCCCAAGACCCAG----- 565
      |||
Qy      301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
      |||
Db      566 -----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 618
      |||
Qy      361 CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTTG 420
      |||
Db      619 CAGGATGTAGGAAGACCCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG 678
      |||
Qy      421 CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACAT 478
      |||
Db      679 CTCTGCACGAGTTACCTGTAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACAT 738
      |||
Qy      479 TTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTTC 523
      |||
Db      739 TTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTTC 784

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Job time : 211.995 secs

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OM nucleic - nucleic search, using sw model

Run on: December 13, 2003, 06:03:55 ; Search time 48.3585 Seconds
(without alignments)
4773.589 Million cell updates/sec

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Perfect score: 523
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	523	100.0	553	3	US-09-142-583A-3
2	523	100.0	553	3	US-09-142-583A-5
3	332.8	63.6	777	3	US-09-142-583A-10
4	331.2	63.3	622	6	5405942-2
5	274.6	52.5	5707	2	US-08-472-809B-8
6	274.6	52.5	6345	2	US-08-472-809B-7
7	234.4	44.8	357	6	5405942-13
8	232.8	44.5	357	6	5405942-9
9	191.4	36.6	210	6	5405942-7
10	191.4	36.6	210	6	5405942-11
11	191.4	36.6	2862	4	US-09-255-829-13

12	189.8	36.3	210	6	5405942-15	Patent No. 5405942
13	185.2	35.4	240	1	US-08-308-196A-1	Sequence 1, Appli
14	185.2	35.4	240	5	PCT-US91-06452-1	Sequence 1, Appli
15	185.2	35.4	390	3	US-09-029-267-13	Sequence 13, Appl
16	158.8	30.4	798	1	US-07-953-230A-6	Sequence 6, Appli
17	154.8	29.6	770	1	US-07-953-230A-1	Sequence 1, Appli
18	154.8	29.6	846	1	US-07-953-230A-5	Sequence 5, Appli
19	127	24.3	621	3	US-08-989-251-40	Sequence 40, Appl
20	127	24.3	621	3	US-09-340-250-40	Sequence 40, Appl
21	127	24.3	621	4	US-09-528-108-40	Sequence 40, Appl
22	125.8	24.1	233	1	US-08-444-142-3	Sequence 3, Appli
23	125.8	24.1	233	1	US-08-444-131-3	Sequence 3, Appli
24	125.8	24.1	485	1	US-07-989-845-29	Sequence 29, Appl
25	125.8	24.1	485	1	US-07-989-844-13	Sequence 13, Appl
26	125.8	24.1	485	1	US-08-110-663-1	Sequence 1, Appli
27	125.8	24.1	485	1	US-08-169-688-1	Sequence 1, Appli
28	125.8	24.1	485	1	US-08-240-121-13	Sequence 13, Appl
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33	125.8	24.1	485	1	US-08-470-108-1	Sequence 1, Appli
34	125.8	24.1	485	5	PCT-US93-11297-13	Sequence 13, Appl
35	125.8	24.1	485	5	PCT-US93-11298-29	Sequence 29, Appl
36	125.6	24.0	243	2	US-08-482-182-75	Sequence 75, Appl
37	124.2	23.7	717	1	US-08-284-784-40	Sequence 40, Appl
38	124.2	23.7	717	2	US-08-854-811-40	Sequence 40, Appl
39	124.2	23.7	783	1	US-08-284-784-43	Sequence 43, Appl
40	124.2	23.7	783	2	US-08-854-811-43	Sequence 43, Appl
41	124.2	23.7	891	1	US-08-284-784-33	Sequence 33, Appl
42	124.2	23.7	891	1	US-08-284-784-34	Sequence 34, Appl
43	124.2	23.7	891	2	US-08-854-811-33	Sequence 33, Appl
44	124.2	23.7	891	2	US-08-854-811-34	Sequence 34, Appl
45	124.2	23.7	900	1	US-08-284-784-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1

US-09-142-583A-3

; Sequence 3, Application US/09142583A

; Patent No. 6221842

; GENERAL INFORMATION:

; APPLICANT: GOLDSPIK, GEOFFREY

; TITLE OF INVENTION: METHOD OF TREATING MUSCULAR DISORDERS

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: NIXON & VANDERHYE P.C.

; STREET: 1100 NORTH GLEBE ROAD

; CITY: ARLINGTON

; STATE: VA

; COUNTRY: USA

; ZIP: 22201

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/142,583A
; FILING DATE: 29-Oct-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/GB97/00658
; FILING DATE: 11-MAR-1997
; APPLICATION NUMBER: GB 9605124.8
; FILING DATE: 11-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B. J.
; REGISTRATION NUMBER: 36663
; REFERENCE/DOCKET NUMBER: 117-263
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 7038164000
; TELEFAX: 7038164100
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 553 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..363
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-142-583A-3

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Query Match          100.0%; Score 523; DB 3; Length 553;
Best Local Similarity 100.0%; Pred. No. 1.6e-154;
Matches 523; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      31 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 90
        |||

Qy      61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
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Qy     181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
        |||
Db     211 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 270
        |||

Qy     241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
        |||
Db     271 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 330
        |||

Qy     301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
        |||

```

Db 331 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 390

QY 361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
 |||

Db 391 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 450

QY 421 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480
 |||

Db 451 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 510

QY 481 CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACATTC 523
 |||

Db 511 CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACATTC 553

RESULT 2

US-09-142-583A-5

; Sequence 5, Application US/09142583A

; Patent No. 6221842

; GENERAL INFORMATION:

; APPLICANT: GOLDSPIK, GEOFFREY

; TITLE OF INVENTION: METHOD OF TREATING MUSCULAR DISORDERS

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: NIXON & VANDERHYE P.C.

; STREET: 1100 NORTH GLEBE ROAD

; CITY: ARLINGTON

; STATE: VA

; COUNTRY: USA

; ZIP: 22201

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/142,583A

; FILING DATE: 29-Oct-1998

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/GB97/00658

; FILING DATE: 11-MAR-1997

; APPLICATION NUMBER: GB 9605124.8

; FILING DATE: 11-MAR-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: SADOFF, B. J.

; REGISTRATION NUMBER: 36663

; REFERENCE/DOCKET NUMBER: 117-263

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 7038164000

; TELEFAX: 7038164100

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 553 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: both

; TOPOLOGY: linear

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;      MOLECULE TYPE: cDNA
;      FEATURE:
;      NAME/KEY: CDS
;      LOCATION: 341..397
;      SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-142-583A-5

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Query Match          100.0%;  Score 523;  DB 3;  Length 553;
Best Local Similarity 100.0%;  Pred. No. 1.6e-154;
Matches 523;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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Qy      1  GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
      |||
Db      31  GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 90

Qy      61  AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
      |||
Db      91  AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 150

Qy     121  ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
      |||
Db     151  ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 210

Qy     181  TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240
      |||
Db     211  TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 270

Qy     241  ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
      |||
Db     271  ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 330

Qy     301  AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
      |||
Db     331  AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 390

Qy     361  CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTTG 420
      |||
Db     391  CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTTG 450

Qy     421  CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 480
      |||
Db     451  CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 510

Qy     481  CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACATTC 523
      |||
Db     511  CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACATTC 553

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RESULT 3

US-09-142-583A-10

; Sequence 10, Application US/09142583A

; Patent No. 6221842

; GENERAL INFORMATION:

; APPLICANT: GOLDSPIK, GEOFFREY

; TITLE OF INVENTION: METHOD OF TREATING MUSCULAR DISORDERS

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

Db	359	TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC	418
Qy	241	ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG	300
Db	419	ATGCCCAAGACCCAG-----	433
Qy	301	AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA	360
Db	434	-----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA	486
Qy	361	CAGGATGTAGGAAGACCCCTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTTG	420
Db	487	CAGGATGTAGGAAGACCCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG	546
Qy	421	CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACAT	478
Db	547	CTCTGCACGAGTTACCTGTAAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACAT	606
Qy	479	TTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTTC	523
Db	607	TTAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTTC	652

5405942-2

APPLICANT: BELL, GRAEME I.; RALL, LESLIE B.; MERRYWEATHER,
JAMES P.
TITLE OF INVENTION: PREPRO INSULIN-LIKE GROWTH FACTORS
I AND II

; CURRENT APPLICATION DATA:

FILING DATE: 16-JUN-1987

APPLICATION NUMBER: 630,557

;SEQ ID NO:2:

5405942-2

Matches 359; Conservative 84; Mismatches 28; Indels 55; Gaps 4;

QY 181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240
 :| |||||:||||| || ||| ||| |||:| |:|:||||| ||||| |||||
 Db 225 UGCGCACCCCUCAAGCCUGCCAAGUCAGCUCGUCUGUCCGUGCCCAGCGCCACACCGAC 284
 QY 241 ATGCCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
 |:||||| |||
 Db 285 AUGCCCCAAGACCCAG----- 299
 QY 301 AGAAGGAAAGGAAGTACATTTGAAGAACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
 |||||:|:|:|:| |||||:|||||:|||||:|||||:|
 Db 300 -----AAGGAAGUACAUUUGAAGAACGCAAGUAGAGGGAGUGCAGGAAACAAGAACUA 352
 QY 361 CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTG 420
 |||||:|:| |||||:|:| |||||:||||| ||||| ||||| |||||:|:|
 Db 353 CAGGAUGUAGGAAGACCCUCCUGAGGAGUGAAGAGUGACAUGCCACCGCAGGAUCCUUG 412
 QY 421 CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAATAAGTTTGATCACAT 478
 |:|:| |||:|:|:|:| |:| ||| ||| |||||:|:|:|:| |:|:|
 Db 413 CUCUGCACGAGUUACCUGUUAACUUUGGAACACCUACCAAAAAUAAGUUUGAUAACAU 472
 QY 479 TTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
 :: |||||: ||| ::| |||||:|||||:|||||:|||||:|
 Db 473 UUAAGGAUGGGCGUUUCCCCCAUGAAAUACACAAGUAAACAUUC 518

RESULT 5

US-08-472-809B-8

; Sequence 8, Application US/08472809B

; Patent No. 5925564

; GENERAL INFORMATION:

; APPLICANT: Schwartz, Robert J.

; APPLICANT: DeMayo, Franco J.

; APPLICANT: O'Malley, Bert W.

; TITLE OF INVENTION: Expression Vector Systems and

; TITLE OF INVENTION: Method of Use

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; STREET: Suite 4700

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071-2066

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/472,809B

; FILING DATE: June 7, 1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/209,846

; FILING DATE: March 9, 1994
 ; APPLICATION NUMBER: 07/789,919
 ; FILING DATE: No. 5925564ember 6, 1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Warburg, Richard J.
 ; REGISTRATION NUMBER: 32,327
 ; REFERENCE/DOCKET NUMBER: 214/212
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (213) 489-1600
 ; TELEFAX: (213) 955-0440
 ; TELEX: 67-3510
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5707 bases
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 US-08-472-809B-8

Query Match 52.5%; Score 274.6; DB 2; Length 5707;
 Best Local Similarity 82.2%; Pred. No. 5.3e-76;
 Matches 351; Conservative 0; Mismatches 24; Indels 52; Gaps 1;

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QY      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
      |||
Db      793 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 852

QY      61 AGGGGCTTTTATTTCAACAAGCCCAAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
      |||
Db      853 AGGGGCTTTTATTTCAACAAGCCCAAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 912

QY      121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
      |||
Db      913 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 972

QY      181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
      |||
Db      973 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 1032

QY      241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
      |||
Db      1033 ATGCCCAAGACCCAG----- 1047

QY      301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
      |||
Db      1048 -----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 1100

QY      361 CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTTG 420
      |||
Db      1101 CAGGATGTAGGAAGACCCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCCCCG 1160

QY      421 CTCTGCA 427
      |||
Db      1161 GGCTGCA 1167

```


RESULT 6

US-08-472-809B-7

; Sequence 7, Application US/08472809B

; Patent No. 5925564

; GENERAL INFORMATION:

; APPLICANT: Schwartz, Robert J.

; APPLICANT: DeMayo, Franco J.

; APPLICANT: O'Malley, Bert W.

; TITLE OF INVENTION: Expression Vector Systems and

; TITLE OF INVENTION: Method of Use

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; STREET: Suite 4700

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071-2066

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/472,809B

; FILING DATE: June 7, 1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/209,846

; FILING DATE: March 9, 1994

; APPLICATION NUMBER: 07/789,919

; FILING DATE: No. 5925564ember 6, 1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard J.

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 214/212

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 6345 bases

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

US-08-472-809B-7

Query Match 52.5%; Score 274.6; DB 2; Length 6345;

Best Local Similarity 82.2%; Pred. No. 5.6e-76;

Matches 351; Conservative 0; Mismatches 24; Indels 52; Gaps 1;

Qy 1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
 |||

```

Db      3702 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 3761
Qy      61 AGGGGCTTTTATTTCAACAAGCCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
      |||
Db      3762 AGGGGCTTTTATTTCAACAAGCCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 3821
Qy      121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
      |||
Db      3822 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 3881
Qy      181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240
      |||
Db      3882 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC 3941
Qy      241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
      |||
Db      3942 ATGCCCAAGACCCAG----- 3956
Qy      301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
      |||
Db      3957 -----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 4009
Qy      361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
      |||
Db      4010 CAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCCCCG 4069
Qy      421 CTCTGCA 427
      |||
Db      4070 GGCTGCA 4076

```

RESULT 7

5405942-13

;Patent No. 5405942

; APPLICANT: BELL, GRAEME I.; RALL, LESLIE B.; MERRYWEATHER,
;JAMES P.

; TITLE OF INVENTION: PREPRO INSULIN-LIKE GROWTH FACTORS
;I AND II

; NUMBER OF SEQUENCES: 16

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/65,673

; FILING DATE: 16-JUN-1987

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 630,557

; FILING DATE: 19-JUL-1984

;SEQ ID NO:13:

; LENGTH: 357

5405942-13

Query Match 44.8%; Score 234.4; DB 6; Length 357;

Best Local Similarity 93.8%; Pred. No. 5.1e-64;

Matches 244; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
      |||
Db      43 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 102

```

```

Qy      61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
      |||
Db      103 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 162

Qy      121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
      |||
Db      163 ACAGGTATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 222

Qy      181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240
      |||
Db      223 TGCACACCCCTCAGGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC 282

Qy      241 ATGCCCAAGACTCAGAAGTA 260
      |||
Db      283 ATGCCCAAGACCCAGAAGGA 302

```

RESULT 8

5405942-9

;Patent No. 5405942

; APPLICANT: BELL, GRAEME I.; RALL, LESLIE B.; MERRYWEATHER,
; JAMES P.

; TITLE OF INVENTION: PREPRO INSULIN-LIKE GROWTH FACTORS
; I AND II

; NUMBER OF SEQUENCES: 16

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/65,673

; FILING DATE: 16-JUN-1987

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 630,557

; FILING DATE: 19-JUL-1984

;SEQ ID NO:9:

; LENGTH: 357

5405942-9

Query Match 44.5%; Score 232.8; DB 6; Length 357;
Best Local Similarity 76.5%; Pred. No. 1.6e-63;
Matches 199; Conservative 44; Mismatches 17; Indels 0; Gaps 0;

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Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTTCGTGTGTGGAGAC 60
      |||
Db      43 GGACCGGAGACGCUCUGCGGGGUGAGCUGGUGGACGCUCUUCAGUUCGUGUGUGGAGAC 102

Qy      61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
      |||
Db      103 AGGGGCUUUUAUUUCAACAAGCCACAGGGUAUGGCUCACAGUCGGAGGGCGCCUCAG 162

Qy      121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
      |||
Db      163 ACAGGUAUCGUGGAUGAGUGCUGUUUCCGAGCUGUGAUCUAAGGAGGCUGGAGAUGUAU 222

Qy      181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240
      :|
Db      223 UGCGCACCCCUCAAGCCUGCCAAGUCAGCUCGUCUGUCCGUGCCCAGCGCCACACCGAC 282

Qy      241 ATGCCCAAGACTCAGAAGTA 260
      |:|

```

Db 283 AUGCCCAAGACCCAGAAGGA 302

RESULT 9

5405942-7

;Patent No. 5405942
; APPLICANT: BELL, GRAEME I.;RALL, LESLIE B.;MERRYWEATHER,
;JAMES P.
; TITLE OF INVENTION: PREPRO INSULIN-LIKE GROWTH FACTORS
;I AND II
; NUMBER OF SEQUENCES: 16
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/65,673
; FILING DATE: 16-JUN-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 630,557
; FILING DATE: 19-JUL-1984
;SEQ ID NO:7:
; LENGTH: 210
5405942-7

Query Match 36.6%; Score 191.4; DB 6; Length 210;
Best Local Similarity 75.1%; Pred. No. 1.2e-50;
Matches 157; Conservative 41; Mismatches 11; Indels 0; Gaps 0;

Qy 1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
| | | | | | | | | | : | : | | | | | : | | | | | : | | : | | : | | : | | : | | | | |
Db 1 GGACCGGAGACGCUCUGCGGGGUGAGCUGGUGGAUGCUCUUCAGUUCGUGUGUGGAGAC 60

Qy 61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
| | | | | : : : : | : : | | | | | | | | | | : | | | : | | | | | : | | | | | | | | | |
Db 61 AGGGGCUUUUAUUAACAACAAGCCACAGGGUAUGGCUCAGCAGUCGGAGGGCGCCUCAG 120

Qy 121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
| | | | | : | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | |
Db 121 ACAGGUAUCGUGGAUGAGUGCGUCUCCGGAGCUGUGAUCUAAGGAGGCUGGAGAUGUAU 180

Qy 181 TGTGCACCCCTCAAGCCGGCAAAGGCAGC 209
: | | | | | | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 181 UGCGCACCCCUCAAGCCUGCCAAGUCAGC 209

RESULT 10

5405942-11

;Patent No. 5405942
; APPLICANT: BELL, GRAEME I.;RALL, LESLIE B.;MERRYWEATHER,
;JAMES P.
; TITLE OF INVENTION: PREPRO INSULIN-LIKE GROWTH FACTORS
;I AND II
; NUMBER OF SEQUENCES: 16
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/65,673
; FILING DATE: 16-JUN-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 630,557
; FILING DATE: 19-JUL-1984
;SEQ ID NO:11:

; LENGTH: 210
5405942-11

Query Match 36.6%; Score 191.4; DB 6; Length 210;
Best Local Similarity 94.7%; Pred. No. 1.2e-50;
Matches 198; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
        |||
Db      1 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

Qy     61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
        |||
Db     61 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 120

Qy    121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
        |||
Db    121 ACAGGTATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 180

Qy    181 TGTGCACCCCTCAAGCCGGCAAAGGCAGC 209
        ||
Db    181 TGCGCACCCCTCAAGCCTGCCAAGTCAGC 209
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RESULT 11

US-09-255-829-13

; Sequence 13, Application US/09255829

; Patent No. 6461617

; GENERAL INFORMATION:

; APPLICANT: Shone, Clifford Charles

; APPLICANT: Quinn, Conrad Padraig

; APPLICANT: Foster, Keith Alan

; TITLE OF INVENTION: Recombinant Toxin Fragments

; NUMBER OF SEQUENCES: 29

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN, & FOX P.L.L.C.

; STREET: 1100 NEW YORK AVENUE, NW, SUITE 600

; CITY: WASHINGTON

; STATE: DC

; COUNTRY: USA

; ZIP: 20005-3934

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/255,829

; FILING DATE: 23-FEB-1999

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/GB97/02273

; FILING DATE: 22-AUG-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/782,893

; FILING DATE: 27-DEC-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: ESMOND, ROBERT W.

```

;     REGISTRATION NUMBER: 32,893
;     REFERENCE/DOCKET NUMBER: 1581.0130002
;     TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 202-371-2600
;     TELEFAX: 202-371-2540
;     INFORMATION FOR SEQ ID NO: 13:
;     SEQUENCE CHARACTERISTICS:
;     LENGTH: 2862 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: double
;     TOPOLOGY: linear
;     MOLECULE TYPE: DNA (genomic)
;     FEATURE:
;     NAME/KEY: CDS
;     LOCATION: 1..2862
US-09-255-829-13

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Query Match          36.6%; Score 191.4; DB 4; Length 2862;
Best Local Similarity 94.7%; Pred. No. 4.8e-50;
Matches 198; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
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Db      2644 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 2703
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Qy      61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGGCACCTCAG 120
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Db      2704 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGGCGCCTCAG 2763
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Qy      121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
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Db      2764 ACAGGTATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 2823
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Qy      181 TGTGCACCCCTCAAGCCGGCAAAGGCAGC 209
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Db      2824 TGCGCACCCCTCAAGCCTGCCAAGTCAGC 2852
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RESULT 12
5405942-15
;Patent No. 5405942
;  APPLICANT: BELL, GRAEME I.;RALL, LESLIE B.;MERRYWEATHER,
;JAMES P.
;  TITLE OF INVENTION: PREPRO INSULIN-LIKE GROWTH FACTORS
;I AND II
;  NUMBER OF SEQUENCES: 16
;  CURRENT APPLICATION DATA:
;  APPLICATION NUMBER: US/07/65,673
;  FILING DATE: 16-JUN-1987
;  PRIOR APPLICATION DATA:
;  APPLICATION NUMBER: 630,557
;  FILING DATE: 19-JUL-1984
;SEQ ID NO:15:
;  LENGTH: 210
5405942-15

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Query Match          36.3%; Score 189.8; DB 6; Length 210;

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; REFERENCE/DOCKET NUMBER: 51875
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)238-0999
; TELEFAX: (619)238-0062
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 240 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 14..232
US-08-308-196A-1

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Query Match          35.4%; Score 185.2; DB 1; Length 240;
Best Local Similarity 91.6%; Pred. No. 1.1e-48;
Matches 196; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

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Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
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Qy      61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGGCACCTCAG 120
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Db      77 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGACGGGCGCCTCAG 136
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Qy      121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
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Qy      181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCT 214
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Db      197 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTTGAT 230
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RESULT 14

PCT-US91-06452-1

; Sequence 1, Application PC/TUS9106452

; GENERAL INFORMATION:

; APPLICANT: Brierley, Russell A.

; APPLICANT: Davis, Geneva R.

; APPLICANT: Holtz, Gregory C.

; APPLICANT: Gleeson, Martin A.

; APPLICANT: Bradley, D. H.

; TITLE OF INVENTION: Production of Insulin-Like Growth

; TITLE OF INVENTION: Factor-1 in Methylophilic Yeast Cells

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Fitch, Even, Tabin & Flannery

; STREET: 135 South LaSalle Street, Suite 900

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60603

; COMPUTER READABLE FORM:


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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/06452
; FILING DATE: 19910409
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/578,728
; FILING DATE: 04-SEP-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 51874
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)552-1311
; TELEFAX: (619)552-0095
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 240 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 14..232
PCT-US91-06452-1

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Query Match          35.4%; Score 185.2; DB 5; Length 240;
Best Local Similarity 91.6%; Pred. No. 1.1e-48;
Matches 196; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

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Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
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Qy     61 AGGGGCTTTTATTTCAACAAGCCCAAGGATACGGCTCCAGCAGTCGGAGGGGCACCTCAG 120
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Qy    121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
      |||
Db    137 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTCGAGATGTAT 196
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Qy    181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCT 214
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Db    197 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTTGAT 230
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RESULT 15

US-09-029-267-13

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; Sequence 13, Application US/09029267
; Patent No. 6107057
; GENERAL INFORMATION:
; APPLICANT: Crawford, Kenneth

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; APPLICANT: Zaror, Isabel
 ; APPLICANT: Innis, Michael
 ; TITLE OF INVENTION: Pichia Secretary Leader for Protein
 ; TITLE OF INVENTION: Expression
 ; NUMBER OF SEQUENCES: 40
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Chiron Corporation
 ; STREET: 4560 Horton Street
 ; CITY: Emeryville
 ; STATE: California
 ; COUNTRY: United States
 ; ZIP: 94608
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/029,267
 ; FILING DATE:
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Chung, Ling-Fong
 ; REGISTRATION NUMBER: 36,482
 ; REFERENCE/DOCKET NUMBER: 1165.100
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (510) 601-2704
 ; TELEFAX: (510) 655-3542
 ; INFORMATION FOR SEQ ID NO: 13:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 390 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: other nucleic acid
 ; DESCRIPTION: /desc = "Synthetic"
 US-09-029-267-13

Query Match 35.4%; Score 185.2; DB 3; Length 390;
 Best Local Similarity 91.6%; Pred. No. 1.5e-48;
 Matches 196; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

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Qy      121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
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Db      280 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTCGAGATGTAT 339
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Qy      181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCT 214
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Db      340 TGCACCCCTCAAGCCTGCCAAGTCAGCTTGAT 373
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Job time : 49.3585 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 13, 2003, 07:29:55 ; Search time 233.512 Seconds
(without alignments)
7443.919 Million cell updates/sec

Title: US-09-852-261-5
Perfect score: 523
Sequence: 1 ggaccggagacgctctgcgg.....aaatacacaagtaaacattc 523

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2201672 seqs, 1661799599 residues

Total number of hits satisfying chosen parameters: 4403344

Minimum DB seq length: 0
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Maximum Match 100%
Listing first 45 summaries

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18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query				
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1	523	100.0	523	9	US-09-852-261-5	Sequence 5, Appli
2	467.4	89.4	517	9	US-09-852-261-1	Sequence 1, Appli
3	409	78.2	471	9	US-09-852-261-13	Sequence 13, Appl
4	356.8	68.2	539	9	US-09-852-261-3	Sequence 3, Appli
5	349.4	66.8	651	15	US-10-161-088-1	Sequence 1, Appli
6	334.4	63.9	7260	10	US-09-919-497-24	Sequence 24, Appl
7	334.4	63.9	7260	10	US-09-880-107-3739	Sequence 3739, Ap
8	334.4	63.9	7260	13	US-09-873-319-707	Sequence 707, App
9	334.4	63.9	7260	13	US-09-960-706-1066	Sequence 1066, Ap
10	334.4	63.9	7260	15	US-10-136-639-4	Sequence 4, Appli
11	332.8	63.6	725	15	US-10-207-655-54	Sequence 54, Appl
12	273.6	52.3	612	13	US-10-251-661-7	Sequence 7, Appli
13	262	50.1	487	9	US-09-852-261-11	Sequence 11, Appl
14	237.6	45.4	318	9	US-09-852-261-9	Sequence 9, Appli
15	228	43.6	462	15	US-10-238-114-1	Sequence 1, Appli
16	209	40.0	286	15	US-10-161-088-3	Sequence 3, Appli
17	193	36.9	210	13	US-09-807-742-18	Sequence 18, Appl
18	191.4	36.6	2862	13	US-10-241-596-13	Sequence 13, Appl
19	187	35.8	4532	10	US-09-930-377B-1	Sequence 1, Appli
20	186.6	35.7	210	10	US-09-930-377B-2	Sequence 2, Appli
21	185.2	35.4	390	15	US-10-179-046-13	Sequence 13, Appl
22	163.8	31.3	516	13	US-10-029-386-5832	Sequence 5832, Ap
23	162.8	31.1	182	13	US-10-029-386-18231	Sequence 18231, A
24	141.6	27.1	213	15	US-10-076-816-9	Sequence 9, Appli
25	141.6	27.1	213	15	US-10-077-381-9	Sequence 9, Appli
26	127	24.3	621	9	US-09-921-398-40	Sequence 40, Appl
27	127	24.3	621	15	US-10-280-826-40	Sequence 40, Appl
28	113.4	21.7	480	9	US-09-921-398-38	Sequence 38, Appl
29	113.4	21.7	480	15	US-10-280-826-38	Sequence 38, Appl
30	101.8	19.5	210	13	US-09-807-742-19	Sequence 19, Appl
31	77.2	14.8	854	10	US-09-954-531-989	Sequence 989, App
c 32	75.4	14.4	447	9	US-09-922-217-917	Sequence 917, App
c 33	75.4	14.4	447	10	US-09-833-263-917	Sequence 917, App
c 34	75.4	14.4	447	14	US-10-025-380-917	Sequence 917, App
c 35	75.2	14.4	437	15	US-10-066-543-663	Sequence 663, App
c 36	75.2	14.4	493	15	US-10-066-543-997	Sequence 997, App
c 37	75.2	14.4	518	15	US-10-066-543-1040	Sequence 1040, Ap
c 38	75.2	14.4	536	15	US-10-066-543-428	Sequence 428, App
39	75.2	14.4	543	15	US-10-136-841-1	Sequence 1, Appli
c 40	75.2	14.4	549	15	US-10-066-543-478	Sequence 478, App
c 41	75.2	14.4	574	9	US-09-922-217-918	Sequence 918, App
c 42	75.2	14.4	574	10	US-09-833-263-918	Sequence 918, App
c 43	75.2	14.4	574	14	US-10-025-380-918	Sequence 918, App
c 44	75.2	14.4	577	15	US-10-066-543-1137	Sequence 1137, Ap
c 45	75.2	14.4	579	15	US-10-066-543-1094	Sequence 1094, Ap

ALIGNMENTS

RESULT 1

US-09-852-261-5

; Sequence 5, Application US/09852261

; Patent No. US20020083477A1

; GENERAL INFORMATION:

; APPLICANT: GOLDSPIK, GEOFFREY

```
; APPLICANT:  TERENGHI, GIORGIO
; TITLE OF INVENTION:  REPAIR OF NERVE DAMAGE
; FILE REFERENCE:  117-351
; CURRENT APPLICATION NUMBER:  US/09/852,261
; CURRENT FILING DATE:  2001-05-10
; PRIOR APPLICATION NUMBER:  GB 0011278.9
; PRIOR FILING DATE:  2000-05-10
; NUMBER OF SEQ ID NOS:  14
; SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH:  523
;   TYPE:  DNA
;   ORGANISM:  Oryctolagus cuniculus
US-09-852-261-5
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Query Match          100.0%;  Score 523;  DB 9;  Length 523;
Best Local Similarity 100.0%;  Pred. No. 1.9e-161;
Matches 523;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
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Db      1  GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60

Qy     61  AGGGGCTTTTATTTCAACAAGCCCAAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
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Db     61  AGGGGCTTTTATTTCAACAAGCCCAAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120

Qy    121  ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
      |||
Db    121  ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy    181  TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240
      |||
Db    181  TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240

Qy    241  ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
      |||
Db    241  ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300

Qy    301  AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
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Db    301  AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360

Qy    361  CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420
      |||
Db    361  CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG 420

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RESULT 2

US-09-852-261-1
; Sequence 1, Application US/09852261
; Patent No. US20020083477A1
; GENERAL INFORMATION:
; APPLICANT: GOLDSPIK, GEOFFREY
; APPLICANT: TERENCE, GIORGIO
; TITLE OF INVENTION: REPAIR OF NERVE DAMAGE
; FILE REFERENCE: 117-351
; CURRENT APPLICATION NUMBER: US/09/852,261
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: GB 0011278.9
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 517
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-852-261-1

Qy	1	GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTTCGTGTGTGGAGAC	60
Db	1	GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTTCGTGTGTGGAGAC	60
Qy	61	AGGGGCTTTTATTTCAACAAGCCCAAGGATACGGCTCCAGCAGTCGGAGGGGCACCTCAG	120
Db	61	AGGGGCTTTTATTTCAACAAGCCCAAGGGTATGGCTCCAGCAGTCGGAGGGGCGCCTCAG	120
Qy	121	ACAGGCATCGTGGATGAGTGCTTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC	180
Db	121	ACAGGCATCGTGGATGAGTGCTTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT	180
Qy	181	TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC	240
Db	181	TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC	240
Qy	241	ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAAATGAAGTCTCAGAGG	300
Db	241	ATGCCCAAGACCCAGAAGTATCAGCCCCCATCTACCAACAAGAACACGAAGTCTCA--G	297
Qy	301	AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA	360
Db	298	AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA	357
Qy	361	CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG	420
Db	358	CAGGATGTA-GAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG	416
Qy	421	CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT	480
Db	417	CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT	476
Qy	481	CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACAT	521


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Db      369 CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACATTT 428

Qy      481 CAAAGATGGCATTTCCTCCCAATGAAATACACAAGTAAACATTTC 523
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RESULT 4

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US-09-852-261-3
; Sequence 3, Application US/09852261
; Patent No. US20020083477A1
; GENERAL INFORMATION:
; APPLICANT: GOLDSPIK, GEOFFREY
; APPLICANT: TERENCE, GIORGIO
; TITLE OF INVENTION: REPAIR OF NERVE DAMAGE
; FILE REFERENCE: 117-351
; CURRENT APPLICATION NUMBER: US/09/852,261
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: GB 0011278.9
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 539
; TYPE: DNA
; ORGANISM: Rattus sp.
US-09-852-261-3

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Query Match          68.2%; Score 356.8; DB 9; Length 539;
Best Local Similarity 82.3%; Pred. No. 9.9e-107;
Matches 436; Conservative 0; Mismatches 87; Indels 7; Gaps 2;

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Qy     61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
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Qy    121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
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Qy    181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
          ||||| || ||||| ||||| ||||| || ||||| ||||||| |||||
Db    181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCATCCGGGCCCAGCGCCACACTGAC 240

Qy    241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
          ||||||||||| ||||| ||||| || ||||||| ||||| || |||||
Db    241 ATGCCCAAGACTCAGAAGTCCCAGCCCCATTCGACACACAAGAAAAGGAAGCTGCAAAGG 300

Qy    301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
          ||||||||||| ||||||||||| ||||||||||| ||||||||||| |||||
Db    301 AGAAGGAAAGGAAGTACACTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA 360

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Qy	241	ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG	300
Db	379	ATGCCCAAGACTCAGAAGTCCCCGTCCCTATCGACAAACAAGAAAACGAAGCTGCAAAGG	438
Qy	301	AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA	360
Db	439	AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGAAGTGCAGGAAACAAGACCTA	498
Qy	361	CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTTTG	420
Db	499	CAGAATGTAGGAGGAGCCTCCACGGAGCAGAAAATGCCACATCACCGCAGGATCCTTTG	558
Qy	421	CTCTGCACAGTTACCTGTAAACATTGGAATACCGGCCA-----AAAAATAAGTTTGATC	474
Db	559	CTGCTTGAGCAACCTGCAAAACATCGAAACACCTACCAAATAACAATAATAAGTCCAATA	618
Qy	475	ACATTTTCAAAGAT-GGCATTTCCCCCAATGAAA	506
Db	619	ACATTACAAAGATGGGCATTTCCCCCAATGAAA	651

US-09-919-497-24

; Patent No. US20020106662A1

; APPLICANT: Mutter, George L.

; FILE REFERENCE: B0801/7225

CURRENT FILING DATE: 2001-07-31

; PRIOR FILING DATE: 2000-07-31

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; SOFTWARE: PatentIn version 3.0
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; LENGTH: 7260

; ORGANISM: Homo sapiens

Query Match 63.9%; Score 334.4; DB 10; Length 7260;
Best Local Similarity 84.6%; Pred. No. 9e-99;
Matches 445; Conservative 0; Mismatches 26; Indels 55; Gaps 4;

Db 311 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 370

Db 371 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 430

Ov 121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Db 431 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 490

```

Qy      181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240
      || |||||
Db      491 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC 550

Qy      241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
      |||||
Db      551 ATGCCCAAGACCCAG----- 565

Qy      301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
      |||||
Db      566 -----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 618

Qy      361 CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTG 420
      |||||
Db      619 CAGGATGTAGGAAGACCCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCCTTG 678

Qy      421 CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACAT 478
      |||||
Db      679 CTCTGCACGAGTTACCTGTAAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACAT 738

Qy      479 TTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTTC 523
      || |||||
Db      739 TTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTTC 784

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RESULT 7

US-09-880-107-3739

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; Sequence 3739, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3739
; LENGTH: 7260
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 X57025
US-09-880-107-3739

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Query Match          63.9%; Score 334.4; DB 10; Length 7260;
Best Local Similarity 84.6%; Pred. No. 9e-99;
Matches 445; Conservative 0; Mismatches 26; Indels 55; Gaps 4;

```

Qy 1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
 |||
 Db 311 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 370
 Qy 61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
 |||
 Db 371 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 430
 Qy 121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
 |||
 Db 431 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 490
 Qy 181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240
 |||
 Db 491 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC 550
 Qy 241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
 |||
 Db 551 ATGCCCAAGACCCAG----- 565
 Qy 301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
 |||
 Db 566 -----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 618
 Qy 361 CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTTG 420
 |||
 Db 619 CAGGATGTAGGAAGACCCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG 678
 Qy 421 CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACAT 478
 |||
 Db 679 CTCTGCACGAGTTACCTGTTAAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACAT 738
 Qy 479 TTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTTC 523
 |||
 Db 739 TTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTTC 784

RESULT 8

US-09-873-319-707

; Sequence 707, Application US/09873319A

; Publication No. US20030134324A1

; GENERAL INFORMATION:

; APPLICANT: Munger, William E.

; APPLICANT: Kulkarni, Prakash

; APPLICANT: Getzenberg, Robert H.

; APPLICANT: Waga, Iwao

; APPLICANT: Yamamoto, Jun

; TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic

; TITLE OF INVENTION: Hyperplasia Using Gene Expression Profiles

; FILE REFERENCE: 44921-5029-US

; CURRENT APPLICATION NUMBER: US/09/873,319A

; CURRENT FILING DATE: 2001-06-05

; EARLIER APPLICATION NUMBER: US 60/223,323

; EARLIER FILING DATE: 2000-08-07

; NUMBER OF SEQ ID NOS: 755

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 707

; LENGTH: 7260
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20030134324A1 X57025
US-09-873-319-707

Query Match 63.9%; Score 334.4; DB 13; Length 7260;
Best Local Similarity 84.6%; Pred. No. 9e-99;
Matches 445; Conservative 0; Mismatches 26; Indels 55; Gaps 4;

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Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
      |||
Db    311 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 370

Qy      61 AGGGGCTTTTATTTCAACAAGCCCAAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
      |||
Db    371 AGGGGCTTTTATTTCAACAAGCCCAAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 430

Qy     121 ACAGGCATCGTGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
      |||
Db    431 ACAGGCATCGTGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 490

Qy     181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240
      |||
Db    491 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC 550

Qy     241 ATGCCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
      |||
Db    551 ATGCCCCAAGACCCAG----- 565

Qy     301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
      |||
Db    566 -----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 618

Qy     361 CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTTG 420
      |||
Db    619 CAGGATGTAGGAAGACCCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG 678

Qy     421 CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACAT 478
      |||
Db    679 CTCTGCACGAGTTACCTGTAAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACAT 738

Qy     479 TTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTC 523
      |||
Db    739 TTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTC 784
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RESULT 9

US-09-960-706-1066

; Sequence 1066, Application US/09960706

; Publication No. US20030134280A1

; GENERAL INFORMATION:

; APPLICANT: Munger, William E.

; TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic Hyperplasia Using

; TITLE OF INVENTION: Gene Expression Profiles

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; FILE REFERENCE: 44921-5029-01US
; CURRENT APPLICATION NUMBER: US/09/960,706
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 60/223,323
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 09/873,319
; PRIOR FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 1124
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1066
; LENGTH: 7260
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20030134280A1 X57025
US-09-960-706-1066
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Query Match          63.9%; Score 334.4; DB 13; Length 7260;
Best Local Similarity 84.6%; Pred. No. 9e-99;
Matches 445; Conservative 0; Mismatches 26; Indels 55; Gaps 4;
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```
Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
      |||
Db      311 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 370

Qy      61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
      |||
Db      371 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 430

Qy      121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
      |||
Db      431 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 490

Qy      181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240
      |||
Db      491 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC 550

Qy      241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
      |||
Db      551 ATGCCCAAGACCCAG----- 565

Qy      301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
      |||
Db      566 -----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 618

Qy      361 CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTTG 420
      |||
Db      619 CAGGATGTAGGAAGACCCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG 678

Qy      421 CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACAT 478
      |||
Db      679 CTCTGCACGAGTTACCTGTTAACTTTGGAACACCTACCAAAAAATAAGTTTGATAACAT 738

Qy      479 TTCAAAGAT-GGCATTTCCCCCAATGAAATACACAAGTAAACATTTC 523
      |||
Db      739 TTAAAAGATGGGCGTTTCCCCCAATGAAATACACAAGTAAACATTTC 784
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RESULT 10

US-10-136-639-4

; Sequence 4, Application US/10136639

; Publication No. US20030072761A1

; GENERAL INFORMATION:

; APPLICANT: LeBowitz, Jonathan

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TARGETING PROTEINS ACROSS THE BLOOD BRAIN

; TITLE OF INVENTION: BARRIER

; FILE REFERENCE: SYM-008

; CURRENT APPLICATION NUMBER: US/10/136,639

; CURRENT FILING DATE: 2002-09-06

; PRIOR APPLICATION NUMBER: US 60/329,650

; PRIOR FILING DATE: 2001-10-16

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 4

; LENGTH: 7260

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-136-639-4

Query Match 63.9%; Score 334.4; DB 15; Length 7260;
Best Local Similarity 84.6%; Pred. No. 9e-99;
Matches 445; Conservative 0; Mismatches 26; Indels 55; Gaps 4;

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Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
          |||
Db      311 GGACCGGAGACGCTCTGCGGGGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 370

Qy      61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
          |||
Db      371 AGGGGCTTTTATTTCAACAAGCCACAGGGTATGGCTCCAGCAGTCGGAGGGCGCCTCAG 430

Qy      121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
          |||
Db      431 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTAAGGAGGCTGGAGATGTAT 490

Qy      181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCAGCGCCACACCGAC 240
          ||
Db      491 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCAGCGCCACACCGAC 550

Qy      241 ATGCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
          |||
Db      551 ATGCCCAAGACCCAG----- 565

Qy      301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
          |||
Db      566 -----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 618

Qy      361 CAGGATGTAGGAAGACCCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCCTTTG 420
          |||
Db      619 CAGGATGTAGGAAGACCCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTTTG 678

Qy      421 CTCTGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAAGTTTGATCACAT 478
          |||

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```

Qy      241 ATGCCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
          |||||
Db      487 ATGCCCCAAGACCCAG----- 501

Qy      301 AGAAGGAAAGGAAGTACATTTGAAGAACACAAGTAGAGGGAGTGCAGGAAACAAGAACTA 360
          |||||
Db      502 -----AAGGAAGTACATTTGAAGAACGCAAGTAGAGGGAGTGCAGGAAACAAGAACTA 554

Qy      361 CAGGATGTAGGAAGACCCTTCTGAGGAGTGAAGAAGGACAGGCCACCGCAGGACCCTT 418
          |||||
Db      555 CAGGATGTAGGAAGACCCTCCTGAGGAGTGAAGAGTGACATGCCACCGCAGGATCCTT 612

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RESULT 13

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US-09-852-261-11
; Sequence 11, Application US/09852261
; Patent No. US20020083477A1
; GENERAL INFORMATION:
;   APPLICANT: GOLDSPIK, GEOFFREY
;   APPLICANT: TERENCE, GIORGIO
;   TITLE OF INVENTION: REPAIR OF NERVE DAMAGE
;   FILE REFERENCE: 117-351
;   CURRENT APPLICATION NUMBER: US/09/852,261
;   CURRENT FILING DATE: 2001-05-10
;   PRIOR APPLICATION NUMBER: GB 0011278.9
;   PRIOR FILING DATE: 2000-05-10
;   NUMBER OF SEQ ID NOS: 14
;   SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
;   LENGTH: 487
;   TYPE: DNA
;   ORGANISM: Rattus sp.
US-09-852-261-11

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Query Match          50.1%; Score 262; DB 9; Length 487;
Best Local Similarity 74.7%; Pred. No. 1.5e-75;
Matches 396; Conservative 0; Mismatches 75; Indels 59; Gaps 3;

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Qy      1  GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
          |||||
Db      1  GGACCGAGACCCCTTTGCGGGGCTGAGCTGGTGGACGCTCTTCAGTTCGTGTGTGGACCA 60

Qy      61  AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCCGAGGGGCACCTCAG 120
          |||||
Db      61  AGGGGCTTTTACTTCAACAAGCCACAGTCTATGGCTCCAGCATTCCGAGGGGCACCACAG 120

Qy      121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
          |||||
Db      121 ACGGGCATTGTGGATGAGTGTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180

Qy      181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
          |||||
Db      181 TGTGTCCGCTGCAAGCCTACAAAGTCAGCTCGTTCCATCCGGGCCCAGCGCCACACTGAC 240

Qy      241 ATGCCCCAAGACTCAGAAGTATCAGCCTCCATCTACCAACAAGAAAATGAAGTCTCAGAGG 300
          |||||
Db      241 ATGCCCCAAGACTCAG----- 255

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Db      181 TGCGCACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCCGTGCCCAGCGCCACACCGAC 240
Qy      241 ATGCCCCAAGACTCAGAAGTA 260
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Db      241 ATGCCCCAAGACCCAGAAGGA 260

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RESULT 15

US-10-238-114-1

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; Sequence 1, Application US/10238114
; Publication No. US20030100073A1
; GENERAL INFORMATION:
; APPLICANT: Merial
; APPLICANT: ANDREONI , Christine Michele
; TITLE OF INVENTION: IGF-1 AS FELINE VACCINE ADJUVANT, IN PARTICULAR AGAINST
FELINE RETROVIRUS
; FILE REFERENCE: 454313-3165.1
; CURRENT APPLICATION NUMBER: US/10/238,114
; CURRENT FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: FR 01 11736
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/318,666
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 462
; TYPE: DNA
; ORGANISM: Felis catus
US-10-238-114-1

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Query Match          43.6%; Score 228; DB 15; Length 462;
Best Local Similarity 92.3%; Pred. No. 2.3e-64;
Matches 240; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

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Qy      1 GGACCGGAGACGCTCTGCGGTGCTGAGCTGGTGGATGCTCTTCAGTTCGTGTGTGGAGAC 60
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Db      145 GGACCAGAGACGCTCTGTGGGGCTGAGTTGGTGGACGCTCTTCAGTTCGTGTGTGGAGAC 204

Qy      61 AGGGGCTTTTATTTCAACAAGCCACAGGATACGGCTCCAGCAGTCGGAGGGCACCTCAG 120
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      205 AGGGGTTTTATTTCAACAAGCCACGGGGTATGGCTCCAGCAGTCGGAGGGCACCTCAG 264

Qy      121 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGAGGCTGGAGATGTAC 180
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      265 ACAGGCATCGTGGATGAGTGCTGCTTCCGGAGCTGTGATCTGAGGCGGCTAGAGATGTAC 324

Qy      181 TGTGCACCCCTCAAGCCGGCAAAGGCAGCCCGCTCCGTCCGTGCCCAGCGCCACACCGAC 240
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      325 TGTGCACCCCTCAAGCCTGCCAAGTCTGCCCGCTCAGTCCGTGCTCAGCGCCACACTGAC 384

Qy      241 ATGCCCCAAGACTCAGAAGTA 260
        ||||| ||||| ||||| |||||
Db      385 ATGCCCCAAGGCTCAGAAGGA 404

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Search completed: December 13, 2003, 11:56:48

Job time : 235.512 secs